DESCRIPTION

PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE

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Cross Reference to Related Application

[0001] This application claims the benefit of U.S. Provisional Application 60/431,494, filed December 6, 2002, which is hereby incorporated by reference in its entirety, including all drawings and tables.

Background of Invention

[0002] The recent explosion in genomic sequencing has deposited a wealth of information in the hands of researchers. However, there is not yet a means to efficiently analyze such data to identify which antigens among many thousands are appropriate targets for vaccine development.

[0003] More than 5000 proteins are expressed during the life cycle of the *Plasmodium* spp. parasite. Subunit vaccines currently in development are based on a single or few antigens and may therefore, elicit too narrow a breadth of response, providing neither optimal protection nor protection on genetically diverse backgrounds. By contrast, to duplicate the protection induced by whole organism vaccination (Good, M.F. & Doolan, D.L. Immune effector mechanisms in malaria. *Curr. Opin. Immunol.* 11, 412-419 (1999)), a malaria vaccine targeting an unprecedented number of parasite-derived proteins through inclusion of their minimal $CD8^+$ and $CD4^+$ T cell epitopes in a multiepitope construct appears to be required. However, the antigens mediating whole organism induced protection are largely unknown.

[0004] Because of various factors, principally related to antigen abundance and immunodominance, not all possible antigens are recognized by natural immunity (Yewdell JW, Bennink JR. Immunodominance in major histocompatibility complex class

I-restricted T lymphocyte responses. *Annu. Rev. Immunol.* **17**, 51-88. (1999)). Various approaches have been proposed for antigen identification, including expression cloning (Kawakami, Y. & Rosenberg, S. A. Immunobiology of human melanoma antigens MART-1 and gp100 and their use for immuno-gene therapy. *Int. Rev. Immunol.* **14**, 173-192 (1997)), elution and mass spectrometry sequencing of naturally processed MHC-bound peptides (Rotzschke, O. *et al.* Isolation and analysis of naturally processed viral peptides as recognized by cytotoxic T cells. *Nature* **348**, 252-254 (1990); van Bleek, G. M. & Nathenson, S. G. Isolation of an endogenously processed immunodominant viral peptide from the class I H-2Kb molecule. *Nature* **348**, 213-216 (1990); Hunt, D. F. *et al.* Peptides presented to the immune system by the murine class II major histocompatibility complex molecule I-Ad. *Science* **256**, 1817-1820 (1992); Cox, A. L. *et al.* Identification of a peptide recognized by five melanoma-specific human cytotoxic T cell lines. *Science* **264**, 716-719 (1994)), *in vitro* testing of pools of overlapping peptides (Kern, F. *et al.* Cytomegalovirus (CMV) Phosphoprotein 65 Makes a Large Contribution to Shaping the T Cell Repertoire in CMV-Exposed Individuals. *J. Infect. Dis.* **185**, 1709-1716 (2002)), and reverse immunogenetics (Davenport, M. P. & Hill, A. V. Reverse immunogenetics: from HLA-disease associations to vaccine candidates. *Mol. Med. Today* **2**, 38-45 (1996); Aidoo, M. *et al.* Identification of conserved antigenic components for a cytotoxic T lymphocyte-inducing vaccine against malaria. *Lancet* **345**, 1003-1007 (1995)). However, these methods suffer from potential problems such as the repeated identification of the same (frequent/dominant) epitope, biases at the level of expansion of T cell populations, and use of clonal/oligoclonal T cells. They also tend to underestimate the complexity of responses, and are not able to analyze a large number of potential targets in the context of multiple HLA types. Finally, none of these approaches easily lends itself towards the daunting task of efficiently analyzing large amounts of genomic sequence data.

Brief Summary

[0005] The subject invention also provides novel *Plasmodium falciparum* antigens that are useful in therapeutic and diagnostic applications. In various aspects, the subject invention provides embodiments such as:

A) isolated and/or purified polynucleotide sequences comprising:

a) a polynucleotide sequence encoding a polypeptide sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

b) a complementary polynucleotide sequence to a polynucleotide sequence encoding a polypeptide sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

c) a polynucleotide sequence having at least about 20% to 99.99% identity to a polynucleotide sequence of A(a) or A(b);

d) a fragment of a polynucleotide sequence according to A(a) or A(b);

e) a polynucleotide sequence encoding a polypeptide as set forth in Table 2, 3, 4, 5, or 6, or a polynucleotide sequence encoding a polypeptide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

f) a polynucleotide sequence encoding a variant of a polypeptide (*e.g.*, a variant polypeptide) selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

g) a polynucleotide sequence encoding a polypeptide fragment of a polypeptide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27, wherein the fragment has substantially the same serologic reactivity as the native polypeptide and/or substantially the same T-cell reactivity as the native polypeptide or fragment;

h) a polynucleotide sequence encoding a fragment of a variant polypeptide of a polypeptide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27, wherein the fragment of the variant polypeptide has substantially the same serologic activity as the native polypeptide or substantially the same T-cell reactivity as the native polypeptide or fragment; or

i) a polynucleotide sequence encoding a multi-epitope construct;

B) primers or detection probes (*e.g.*, fragments of the disclosed polynucleotide sequences) for hybridization with a target sequence or the amplicon generated from the target sequence comprising a sequence of at least 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 consecutive nucleotides of the polynucleotide sequences set forth herein. Labeled probes or primers are labeled with a radioactive compound or with another type of label as set forth in embodiment C, below;

C) isolated polynucleotides according to embodiments A or B further comprising a label; labels can include, and are not limited to 1) radioactive labels, 2) enzyme labels, 3) chemiluminescent labels, 4) fluorescent labels, 5) magnetic labels, or other suitable labels. Exemplary labels include, and are not limited to, ^{32}P, ^{35}S, ^{3}H, ^{125}I, biotin, acetylaminofluorene, digoxigenin, 5-bromo-deoxyuridine, or fluorescein;

D) methods of detecting *P. falciparum* in biological samples comprising contacting a biological sample with isolated polynucleotides of embodiments A, B, or C. In this embodiment, *P. falciparum* cells, or cells comprising (infected) by *P. falciparum* are recovered, lysed, and DNA and/or RNA are extracted from the lysed cells. The extracted DNA or RNA is then tested using polynucleotides and/or probes set forth herein for the presence of *P. falciparum*. Typical assay formats utilizing nucleic acid hybridization includes, and are not limited to, 1) nuclear run-on assay, 2) slot blot assay, 3) northern blot assay (Alwine, *et al.* Proc. Natl. Acad. Sci. 74:5350), 4) magnetic particle separation, 5) nucleic Acid or DNA chips, 6) reverse Northern blot assay, 7) dot blot assay, 8) in situ hybridization, 9) RNase protection assay (Melton, *et al.* Nuc. Acids Res. 12:7035 and as described in the 1998 catalog of Ambion, Inc., Austin, Tex.), 10) ligase chain reaction, 11) polymerase chain reaction (PCR), 12) reverse transcriptase (RT)-PCR (Berchtold, *et al.* Nuc. Acids. Res. 17:453), 13) differential display RT-PCR (DDRT-PCR) or other suitable combinations of techniques and assays;

E) analytical systems, such as DNA chips comprising polynucleotide sequences according to embodiments A, B, or C;

F) modified polynucleotide sequences comprising polynucleotide sequences according to embodiments A or B;

G) a polynucleotide sequence according to embodiments A, B, or F, further comprising regulatory sequences, such as promoters, enhancer elements, or termination sequences, that are operably linked to the polynucleotide sequences of embodiments A or B;

H) a vector comprising a promoter operably linked to a nucleic acid sequence of the subject invention (*e.g.*, as set forth in embodiments A, B, or F), optionally, one or more origins of replication, and, optionally, one or more selectable markers (*e.g.*, an antibiotic resistance gene);

I) host cells transformed by a vector according embodiment G or H. The host cell may be chosen from eukaryotic or prokaryotic systems, such as for example bacterial cells, (Gram negative or Gram positive), yeast cells, animal cells (such as Chinese hamster ovary (CHO) cells), plant cells, and/or insect cells using baculovirus vectors. In some embodiments, the host cells for expression of the polypeptides include, and are not limited to, those taught in U.S. Patent Nos. 6,319,691, 6,277,375, 5,643,570, or 5,565,335, each of which is incorporated by reference in its entirety, including all references cited within each respective patent.

I) novel compositions comprising a pharmaceutically acceptable carrier and a polynucleotide according to embodiments A or B;

J) methods of inducing an immune response or protective immune response in an individual comprising the administration of a composition comprising a polynucleotide according to embodiments A and/or B and a

pharmaceutically acceptable carrier in an amount sufficient to induce an immune response;

K) the method according to embodiment J, further comprising the administration of: 1) a viral vector comprising a polynucleotide according to embodiment A and/or B (or composition comprising the viral vector); and/or 2) a polypeptide antigen (or composition thereof) of the invention; in a preferred embodiment, the antigen is the polypeptide that is encoded by the polynucleotide administered as the polynucleotide vaccine. As a particularly preferred embodiment, the polypeptide antigen is administered as a booster subsequent to the initial administration of the polynucleotide vaccine. Exemplary viral vectors suitable for use in this embodiment include, but are not limited to, poxvirus such as vaccinia virus, avipox virus, fowlpox virus, a highly attenuated vaccinia virus (such as Ankara or MVA [Modified Vaccinia Ankara]), retrovirus, adenovirus, baculovirus and the like. In a preferred embodiment, the viral vector is Ankara or MVA;

L) compositions comprising the polynucleotides of embodiments A, B, or F inserted into nucleic acid vaccine vectors (plasmids) or viral vectors and, optionally, a pharmaceutically acceptable carrier, *e.g.*, saline;

M) one or more isolated polypeptides comprising:

a) a polypeptide encoded by a polynucleotide sequence according to embodiment A(a);

b) a variant polypeptide encoded by a polynucleotide sequence having at least about 20% to 99.99% identity to a polynucleotide according to embodiment A(a);

c) a fragment of a polypeptide or a variant polypeptide, wherein said fragment or variant has substantially the same serologic reactivity or substantially the same T-cell reactivity as the native polypeptide (*e.g.*, those polypeptides set forth in SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27 and Tables 2, 3, 4, 5 or 6);

d) a polypeptide sequence provided in Tables 2, 3, 4, 5 or 6 or selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

e) a variant polypeptide having at least about 20% to 99.99% identity to a polypeptide provided in Tables 2, 3, 4, 5 or 6 or selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

f) a polypeptide (epitope) set forth in Table 2, 3, 4, 5 or 6; or

g) a multi-epitope construct: 1) comprising at least one epitope set forth in Table 2, 3, 4, 5 or 6; 2) comprising a polypeptide selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27 and at least one epitope set forth in Tables 2, 3, 4, 5 and/or 6; or 3) comprising and at least one epitope set forth in Tables 2, 3, 4, 5 and/or 6 and one or more polypeptide selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

N) a polypeptide epitope according to embodiment M(f), wherein the polypeptide epitope is a CTL-inducing peptides of about 13 residues or less in length, preferably between about 8 and about 11 residues (*e.g.*, 8, 9, 10 or all residues), and more preferably 9 or 10 residues;

O) a polypeptide epitope according to embodiment M(f), wherein the polypeptide epitope is a HTL-inducing peptide of less than about 50 residues, preferably, between about 6 and about 30 residues, more preferably, between about 12 and 25 residues (*e.g.*, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 residues), and most preferably, between about 15 and 20 residues (*e.g.*, 15, 16, 17, 18, 19, or 20 residues);

P) methods for eliciting an immune response in an individual comprising the administration of compositions comprising polypeptides according

to embodiment M or N to an individual in amounts sufficient to induce an immune response in the individual;

Q) a composition comprising a pharmaceutically acceptable carrier and a polypeptide according to embodiment M or N, that can, optionally, contain an adjuvant;

R) diagnostic assays based upon Western blot formats, or standard immunoassays known to the skilled artisan, comprising contacting a biological sample obtained from an individual with a polypeptide according to the embodiments M or N and detecting the formation of an antibody-antigen complex or detecting the stimulation of T-cells obtained from the individual (for example, as set forth in the Examples herein);

S) a "multi-epitope construct" comprising: 1) polynucleotides that encode multiple polypeptide epitopes (of any length) that can bind to one or more molecules functioning in the immune system; or 2) polypeptides comprising multiple polypeptide epitopes that can bind to one or more molecules functioning in the immune system. Some embodiments provide for "multi-epitope constructs" that comprise a combination or series of different epitopes, optionally connected by "flanking" residues. "Multi-epitope constructs" can include the full length polypeptides from which the epitopes are obtained (*e.g.*, the polypeptides of SEQ ID NOs: 1-27);

T) a multi-epitope construct according to embodiment S, wherein the epitopes used in the formation of the multi-epitope construct are selected from those set forth in Table 2, Table, 3, Table 4, Table 5, and Table 6;

U) a multi-epitope construct according to embodiments S or T that is of "high affinity" or "intermediate affinity";

V) a multi-epitope construct according to embodiments S, T, or U that comprises five or more, ten or more, fifteen or more, twenty or more, or twenty-

five or more epitopes. Other embodiments provide multi-epitope constructs that comprise at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 epitopes.

W) a multi-epitope construct according to embodiments S, T, U, or V wherein: a) all of the epitopes in a multi-epitope construct are from one organism (*e.g.*, the epitopes are obtained from *P. falciparum*); or b) or the multi-epitope construct includes epitopes present in two or more different organisms (*e.g.*, some epitopes from *P. falciparum* and some epitopes from another organism). Additionally, the same epitope may be present in a multi-epitope construct at more than one location in the construct. In some embodiments, novel epitopes of the subject invention may be linked to known epitopes of an organism (*e.g., P. falciparum* or another organism).

X) a multi-epitope construct according to embodiments S, T, U, V, or W, wherein the individual epitopes interact with an antigen binding site of an antibody molecule or fragment thereof, a class I HLA, a T-cell receptor, and/or a class II HLA molecule.

Y) a multi-epitope construct according to embodiments S, T, U, V, W, or X, wherein the construct further comprises, optionally, 1 to 5 "flanking" or "linking" residues positioned next to one or more epitopes;

Z) a multi-epitope construct according to embodiments S, T, U, V, W, X, or Y that has, optionally, been "optimized";

AA) an isolated antibody or fragment thereof that specifically binds to a polypeptide as set forth in embodiments M or N;

BB) a viral vector comprising a polynucleotide according to embodiment A or B. Exemplary viral vectors suitable for use in this embodiment include, but are not limited to, poxvirus such as vaccinia virus, avipox virus, fowlpox virus, a highly attenuated vaccinia virus (such as Ankara or MVA [Modified Vaccinia Ankara]), retrovirus, adenovirus, baculovirus and the like. In a preferred embodiment, the viral vector is Ankara or MVA; and/or

CC) a viral vector according to embodiment BB, wherein the viral vector further comprises nucleic acids encoding immunostimulatory molecules such as IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-15, Il-16, Il-18, IL-23, IL-24, erythropoietin, G-CSF, M-CSF, platelet derived growth factor (PDGF), MSF, FLT-3 ligand, EGF, fibroblast growth factor (FGF; *e.g.*, aFGF (FGF-1), bFGF (FGF-2), FGF-3, FGF-4, FGF-5, FGF-6, or FGF-7), insulin-like growth factors (*e.g.*, IGF-1, IGF-2); vascular endothelial growth factor (VEGF); interferons (*e.g.*, IFN-γ, IFN-α, IFN-β); leukemia inhibitory factor (LIF); ciliary neurotrophic factor (CNTF); oncostatin M; stem cell factor (SCF); transforming growth factors (*e.g.*, TGF-α, TGF-β1, TGF-β1, TGF-β1), or chemokines (such as, but not limited to, BCA-1/BLC-1, BRAK/Kec, CXCL16, CXCR3, ENA-78/LIX, Eotaxin-1, Eotaxin-2/MPIF-2, Exodus-2/SLC, Fractalkine/Neur7otactin, GROalpha/MGSA, HCC-1, I-TAC, Lymphotactin/ATAC/SCM, MCP-1/MCAF, MCP-3, MCP-4, MDC/STCP-1, ABCD-1, MIP-1α, MIP-1β, MIP-2α/GROβ, MIP-3α/Exodus/LARC, MIP-3β/Exodus-3/ELC, MIP-4/PARC/DC-CK1, PF-4, RANTES, SDF1α, TARC, or TECK).

Brief Description of Drawings and Tables

[0006] Table 1 presents a summary of immune reactivities of a panel of 27 novel antigens and four known antigens.

[0007] Tables 2-6 provide peptide epitopes of *P. falciparum.*

Brief Description of Sequences

[0008] Sequence ID NOs: 1-27 are amino acid sequences of novel malaria antigens.

Detailed Disclosure

[0009] The subject invention provides isolated and/or purified novel *P. falciparum* polynucleotides and fragments of these novel polynucleotides. Thus, the present invention provides isolated and/or purified polynucleotide sequences comprising:

a) a polynucleotide sequence encoding a polypeptide sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

b) a complementary polynucleotide sequence to a polynucleotide sequence encoding a polypeptide sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

c) a polynucleotide sequence having at least about 20% to 99.99% identity to a polynucleotide sequence of (a) or (b);

d) a fragment of a polynucleotide sequence according to (a) or (b);

e) a polynucleotide sequence encoding a polypeptide as set forth in Table 2, 3, 4, 5 or 6 or a polynucleotide sequence encoding a polypeptide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

f) a polynucleotide sequence encoding variant of a polypeptide (*e.g.*, a variant polypeptide) selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

g) a polynucleotide sequence encoding a polypeptide fragment of a polypeptide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27, wherein the fragment has substantially the same serologic reactivity as the native polypeptide or

substantially the same T-cell reactivity as the native polypeptide or fragment;

h) a polynucleotide sequence encoding a fragment of a variant polypeptide of a polypeptide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27, wherein the fragment of the variant polypeptide has substantially the same serologic activity as the native polypeptide or substantially the same T-cell reactivity as the native polypeptide or fragment; or

i) a polynucleotide sequence encoding a multi-epitope construct.

[0010] "Nucleotide sequence", "polynucleotide" or "nucleic acid" can be used interchangeably and are understood to mean, according to the present invention, either a double-stranded DNA, a single-stranded DNA or products of transcription of the said DNAs (*e.g.*, RNA molecules). It should also be understood that the present invention does not relate to genomic polynucleotide sequences of *P. falciparum* in their natural environment or natural state. The nucleic acid, polynucleotide, or nucleotide sequences of the invention have been isolated, purified (or partially purified), by separation methods including, but not limited to, ion-exchange chromatography, molecular size exclusion chromatography, affinity chromatography, or by genetic engineering methods such as amplification, cloning, subcloning or chemical synthesis.

[0011] A homologous polynucleotide or polypeptide sequence, for the purposes of the present invention, encompasses a sequence having a percentage identity with the polynucleotide or polypeptide sequences, set forth herein, of between at least (or at least about) 20.00% to 99.99% (inclusive). The aforementioned range of percent identity is to be taken as including, and providing written description and support for, any fractional percentage, in intervals of 0.01%, between 20.00% and, up to, including 99.99%. These percentages are purely statistical and differences between two nucleic acid sequences can be distributed randomly and over the entire sequence length.

[0012] In various embodiments, homologous sequences can exhibit a percent identity of 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 percent with the sequences of the instant invention. Typically, the percent identity is calculated with reference to the full length, native, and/or naturally occurring polypeptide or polynucleotide (*e.g.*, those polypeptides set forth in SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27 or those set forth in SEQ ID NOs:28-81)). The terms "identical" or percent "identity", in the context of two or more polynucleotide or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues that are the same, when compared and aligned for maximum correspondence over a comparison window, as measured using a sequence comparison algorithm or by manual alignment and visual inspection. Preferably, such a substitution is made in accordance with analoging principles set forth, *e.g.*, in co-pending U.S. Ser. No. 09/260,714 filed Mar. 1, 1999 and 09/226,775, filed January 6, 1999 and PCT application number PCT/US00/19774 each of which is hereby incorporated by reference in its entirety.

[0013] Both protein and nucleic acid sequence homologies may be evaluated using any of the variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to, TBLASTN, BLASTP, FASTA, TFASTA, and CLUSTALW (Pearson and Lipman, 1988, *Proc. Natl. Acad. Sci. USA 85(8)*:2444-2448; Altschul *et al.*, 1990, *J. Mol. Biol. 215(3)*:403-410; Thompson *et al.*, 1994, *Nucleic Acids Res. 22(2)*:4673-4680; Higgins *et al.*, 1996, *Methods Enzymol. 266*:383-402; Altschul *et al.*, 1990, *J. Mol. Biol. 215(3)*:403-410; Altschul *et al.*, 1993, *Nature Genetics 3*:266-272). Sequence comparisons are, typically, conducted using default parameters provided by the vendor or using those parameters set forth in the above-identified references, which are hereby incorporated by reference in their entireties.

[0014] A "complementary" polynucleotide sequence, as used herein, generally refers to a sequence arising from the hydrogen bonding between a particular purine and a particular pyrimidine in double-stranded nucleic acid molecules (DNA-DNA, DNA-

RNA, or RNA-RNA). The major specific pairings are guanine with cytosine and adenine with thymine or uracil. A "complementary" polynucleotide sequence may also be referred to as an "antisense" polynucleotide sequence or an "antisense" sequence.

[0015] Sequence homology and sequence identity can also be determined by hybridization studies under high stringency, intermediate stringency, and/or low stringency. Various degrees of stringency of hybridization can be employed. The more severe the conditions, the greater the complementarity that is required for duplex formation. Severity of conditions can be controlled by temperature, probe concentration, probe length, ionic strength, time, and the like. Preferably, hybridization is conducted under low, intermediate, or high stringency conditions by techniques well known in the art, as described, for example, in Keller, G.H., M.M. Manak [1987] *DNA Probes*, Stockton Press, New York, NY, pp. 169-170.

[0016] For example, hybridization of immobilized DNA on Southern blots with ^{32}P-labeled gene-specific probes can be performed by standard methods (Maniatis *et al.* [1982] *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York). In general, hybridization and subsequent washes can be carried out under intermediate to high stringency conditions that allow for detection of target sequences with homology to the exemplified polynucleotide sequence. For double-stranded DNA gene probes, hybridization can be carried out overnight at 20-25° C below the melting temperature (T_m) of the DNA hybrid in 6X SSPE, 5X Denhardt's solution, 0.1% SDS, 0.1 mg/ml denatured DNA. The melting temperature is described by the following formula (Beltz *et al.* [1983] *Methods of Enzymology*, R. Wu, L. Grossman and K. Moldave [eds.] Academic Press, New York 100:266-285).

[0017] $Tm=81.5°C+16.6\ Log[Na^+]+0.41(\%G+C)-0.61(\%formamide)-600/length$ of duplex in base pairs.

[0018] Washes are typically carried out as follows:

(1) twice at room temperature for 15 minutes in 1X SSPE, 0.1% SDS (low stringency wash);

(2) once at T_m - 20°C for 15 minutes in 0.2X SSPE, 0.1% SDS (intermediate stringency wash).

[0019] For oligonucleotide probes, hybridization can be carried out overnight at 10-20°C below the melting temperature (T_m) of the hybrid in 6X SSPE, 5X Denhardt's solution, 0.1% SDS, 0.1 mg/ml denatured DNA. T_m for oligonucleotide probes can be determined by the following formula:

[0020] T_m (°C)=2(number T/A base pairs)+4(number G/C base pairs) (Suggs *et al.* [1981] *ICN-UCLA Symp. Dev. Biol. Using Purified Genes*, D.D. Brown [ed.], Academic Press, New York, 23:683-693).

[0021] Washes can be carried out as follows:

(1) twice at room temperature for 15 minutes 1X SSPE, 0.1% SDS (low stringency wash);

2) once at the hybridization temperature for 15 minutes in 1X SSPE, 0.1% SDS (intermediate stringency wash).

[0022] In general, salt and/or temperature can be altered to change stringency. With a labeled DNA fragment >70 or so bases in length, the following conditions can be used:

Low:	1 or 2X SSPE, room temperature
Low:	1 or 2X SSPE, 42°C
Intermediate:	0.2X or 1X SSPE, 65°C
High:	0.1X SSPE, 65°C.

[0023] By way of another non-limiting example, procedures using conditions of high stringency can also be performed as follows: Pre-hybridization of filters containing DNA is carried out for 8 h to overnight at 65°C in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65°C, the preferred hybridization temperature, in pre-hybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 x 10^6 cpm of ^{32}P-labeled probe. Alternatively, the hybridization step can be performed at 65°C in the presence of SSC buffer, 1X SSC

corresponding to 0.15M NaCl and 0.05 M Na citrate. Subsequently, filter washes can be done at 37°C for 1 h in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1X SSC at 50°C for 45 min. Alternatively, filter washes can be performed in a solution containing 2X SSC and 0.1% SDS, or 0.5X SSC and 0.1% SDS, or 0.1X SSC and 0.1% SDS at 68°C for 15 minute intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. Other conditions of high stringency which may be used are well known in the art and as cited in Sambrook *et al.*, 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel *et al.*, 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety.

[0024] Another non-limiting example of procedures using conditions of intermediate stringency are as follows: Filters containing DNA are pre-hybridized, and then hybridized at a temperature of 60°C in the presence of a 5X SSC buffer and labeled probe. Subsequently, filters washes are performed in a solution containing 2X SSC at 50°C and the hybridized probes are detectable by autoradiography. Other conditions of intermediate stringency which may be used are well known in the art and as cited in Sambrook *et al.*, 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel *et al.*, 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety.

[0025] Duplex formation and stability depend on substantial complementarity between the two strands of a hybrid and, as noted above, a certain degree of mismatch can be tolerated. Therefore, the probe sequences of the subject invention include mutations (both single and multiple), deletions, insertions of the described sequences, and combinations thereof, wherein said mutations, insertions and deletions permit formation of stable hybrids with the target polynucleotide of interest. Mutations, insertions and deletions can be produced in a given polynucleotide sequence in many ways, and these methods are known to an ordinarily skilled artisan. Other methods may become known in the future.

[0026] It is also well known in the art that restriction enzymes can be used to obtain functional fragments of the subject DNA sequences. For example, *Bal*31

exonuclease can be conveniently used for time-controlled limited digestion of DNA (commonly referred to as "erase-a-base" procedures). See, for example, Maniatis *et al.* [1982] *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York; Wei *et al.* [1983] *J. Biol. Chem.* 258:13006-13512.

[0027] The present invention further comprises fragments of the polynucleotide sequences of the instant invention. Representative fragments of the polynucleotide sequences according to the invention will be understood to mean any nucleotide fragment having at least 8 successive nucleotides, preferably at least 12 successive nucleotides, and still more preferably at least 15 or at least 20 successive nucleotides of the sequence from which it is derived. The upper limit for such fragments is the total number of polynucleotides found in the full length sequence (or, in certain embodiments, of the full length open reading frame (ORF) identified herein).

[0028] In some embodiments, the subject invention includes those fragments capable of hybridizing under various conditions of stringency conditions (*e.g.*, high or intermediate or low stringency) with a nucleotide sequence according to the invention; fragments that hybridize with a nucleotide sequence of the subject invention can be, optionally, labeled as set forth below.

[0029] Other embodiments provide for nucleic acid fragments corresponding to nucleotide sequences comprising full, or partial, open reading frames (ORF sequences). Also within the scope of the invention are those polynucleotide fragments encoding polypeptides reactive with antibodies found in the serum of individuals infected with *P. falciparum*. Fragments according to the subject invention can be obtained, for example, by specific amplification (*e.g.*, PCR amplification), digestion with restriction enzymes, of nucleotide sequences according to the invention. Such methodologies are well-known in the art and are taught, for example, by Sambrook *et al.*, 1989. Nucleic acid fragments according to the invention can also be obtained by chemical synthesis according to methods well known to persons skilled in the art.

[0030] The subject invention also provides nucleic acid based methods for the identification of the presence of an organism in a sample. In these varied embodiments, the invention provides for the detection of nucleic acids in a sample comprising contacting a sample with a nucleic acid (polynucleotide) of the subject invention (such as

an RNA, mRNA, DNA, cDNA, or other nucleic acid). In a preferred embodiment, the polynucleotide is a probe that is, optionally, labeled and used in the detection system. Many methods for detection of nucleic acids exist and any suitable method for detection is encompassed by the instant invention. Typical assay formats utilizing nucleic acid hybridization includes, and are not limited to, 1) nuclear run-on assay, 2) slot blot assay, 3) northern blot assay (Alwine, *et al.* Proc. Natl. Acad. Sci. 74:5350), 4) magnetic particle separation, 5) nucleic Acid or DNA chips, 6) reverse Northern blot assay, 7) dot blot assay, 8) in situ hybridization, 9) RNase protection assay (Melton, *et al.* Nuc. Acids Res. 12:7035 and as described in the 1998 catalog of Ambion, Inc., Austin, Tex.), 10) ligase chain reaction, 11) polymerase chain reaction (PCR), 12) reverse transcriptase (RT)-PCR (Berchtold, *et al.* Nuc. Acids. Res. 17:453), 13) differential display RT-PCR (DDRT-PCR) or other suitable combinations of techniques and assays. Labels suitable for use in these detection methodologies include, and are not limited to 1) radioactive labels, 2) enzyme labels, 3) chemiluminescent labels, 4) fluorescent labels, 5) magnetic labels, or other suitable labels, including those set forth below. These methodologies and labels are well known in the art and widely available to the skilled artisan. Likewise, methods of incorporating labels into the nucleic acids are also well known to the skilled artisan.

[0031] Thus, the subject invention also provides detection probes (*e.g.*, fragments of the disclosed polynucleotide sequences) for hybridization with a target sequence or the amplicon generated from the target sequence. Such a detection probe will advantageously have as sequence a sequence of at least 8, 9, 10, 11, 12, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 nucleotides. Labeled probes or primers are labeled with a radioactive compound or with another type of label as set forth above. Alternatively, non-labeled nucleotide sequences may be used directly as probes or primers; however, the sequences are generally labeled with a radioactive element (^{32}P, ^{35}S, ^{3}H, ^{125}I) or with a molecule such as biotin, acetylaminofluorene, digoxigenin, 5-bromo-deoxyuridine, or fluorescein to provide probes that can be used in numerous applications.

[0032] The polynucleotide sequences according to the invention may also be used in analytical systems, such as DNA chips. DNA chips and their uses are well known in the art and (see for example, U.S. Patent Nos. 5,561,071; 5,753,439; 6,214,545; *Schena et al.*, BioEssays, 1996, 18:427-431; *Bianchi et al.*, Clin. Diagn. Virol., 1997, 8:199-208;

each of which is hereby incorporated by reference in their entireties) and/or are provided by commercial vendors such as Affymetrix, Inc. (Santa Clara, CA). In addition, the nucleic acid sequences of the subject invention can be used as molecular weight markers in nucleic acid analysis procedures.

[0033] The subject invention also provides for modified nucleotide sequences. Modified nucleic acid sequences will be understood to mean any nucleotide sequence that has been modified, according to techniques well known to persons skilled in the art, and exhibiting modifications in relation to the native, naturally occurring nucleotide sequences. One non-limiting example of a "modified" nucleotide sequences includes mutations in regulatory and/or promoter sequences of a polynucleotide sequence that result in a modification of the level of expression of the polypeptide. A "modified" nucleotide sequence will also be understood to mean any nucleotide sequence encoding a "modified" polypeptide as defined below.

[0034] Another aspect of the invention provides vectors for the cloning and/or the expression of a polynucleotide sequence taught herein. Vectors of this invention, including vaccine vectors, can also comprise elements necessary to allow the expression and/or the secretion of the said nucleotide sequences in a given host cell. The vector can contain a promoter, signals for initiation and for termination of translation, as well as appropriate regions for regulation of transcription. In certain embodiments, the vectors can be stably maintained in the host cell and can, optionally, contain signal sequences directing the secretion of translated protein. These different elements are chosen according to the host cell used. Vectors can integrate into the host genome or, optionally, be autonomously-replicating vectors.

[0035] The subject invention also provides for the expression of a polypeptide, peptide, derivative, or variant encoded by a polynucleotide sequence disclosed herein comprising the culture of an organism transformed with a polynucleotide of the subject invention under conditions that allow for the expression of the polypeptide, peptide, derivative, or analog and, optionally, recovering the expressed polypeptide, peptide, derivative, or analog.

[0036] The disclosed polynucleotide sequences can also be regulated by a second nucleic acid sequence so that the protein or peptide is expressed in a host transformed

with the recombinant DNA molecule. For example, expression of a protein or peptide may be controlled by any promoter/enhancer element known in the art. Promoters which may be used to control expression include, but are not limited to, the CMV-IE promoter, the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, *et al.*, 1980, Cell 22:787-797), the herpes simplex thymidine kinase promoter (Wagner *et al.*, 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster *et al.*, 1982, Nature 296:39-42); prokaryotic vectors containing promoters such as the β-lactamase promoter (Villa-Kamaroff, *et al.*, 1978, Proc. Natl. Acad. Sci. U.S.A. 75:3727-3731), or the *tac* promoter (DeBoer, *et al.*, 1983, Proc. Natl. Acad. Sci. U.S.A. 80:21-25); see also "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242:74-94; plant expression vectors comprising the nopaline synthetase promoter region (Herrera-Estrella *et al.*, 1983, Nature 303:209-213) or the cauliflower mosaic virus 35S RNA promoter (Gardner, *et al.*, 1981, Nucl. Acids Res. 9:2871), and the promoter of the photosynthetic enzyme ribulose biphosphate carboxylase (Herrera-Estrella *et al.*, 1984, Nature 310:115-120); promoter elements from yeast or fungi such as the Gal 4 promoter, the ADC (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, and/or the alkaline phosphatase promoter.

[0037] The vectors according to the invention are, for example, vectors of plasmid or viral origin. In a specific embodiment, a vector is used that comprises a promoter operably linked to a protein or peptide-encoding nucleic acid sequence contained within the disclosed polynucleotide sequences, one or more origins of replication, and, optionally, one or more selectable markers (*e.g.*, an antibiotic resistance gene). Expression vectors comprise regulatory sequences that control gene expression, including gene expression in a desired host cell. Exemplary vectors for the expression of the polypeptides of the invention include the pET-type plasmid vectors (Promega) or pBAD plasmid vectors (Invitrogen) or those provided in the examples below. Furthermore, the vectors according to the invention are useful for transforming host cells so as to clone or express the polynucleotide sequences of the invention.

[0038] The invention also encompasses the host cells transformed by a vector according to the invention. These cells may be obtained by introducing into host cells a nucleotide sequence inserted into a vector as defined above, and then culturing the said

cells under conditions allowing the replication and/or the expression of the polynucleotide sequences of the subject invention.

[0039] The host cell may be chosen from eukaryotic or prokaryotic systems, such as for example bacterial cells, (Gram negative or Gram positive), yeast cells (for example, *Saccharomyces cereviseae* or *Pichia pastoris*), animal cells (such as Chinese hamster ovary (CHO) cells), plant cells, and/or insect cells using baculovirus vectors. In some embodiments, the host cells for expression of the polypeptides include, and are not limited to, those taught in U.S. Patent Nos. 6,319,691, 6,277,375, 5,643,570, or 5,565,335, each of which is incorporated by reference in its entirety, including all references cited within each respective patent.

[0040] Furthermore, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Expression from certain promoters can be elevated in the presence of certain inducers; thus, expression of the genetically engineered polypeptide may be controlled. Furthermore, different host cells have characteristic and specific mechanisms for the translational and post-translational processing and modification (*e.g.*, glycosylation, phosphorylation) of proteins. Appropriate cell lines or host systems can be chosen to ensure the desired modification and processing of the foreign protein expressed. For example, expression in a bacterial system can be used to produce an unglycosylated core protein product. Expression in yeast will produce a glycosylated product. Expression in mammalian cells can be used to ensure "native" glycosylation of a heterologous protein. Furthermore, different vector/host expression systems may effect processing reactions to different extents.

[0041] The subject invention also concerns novel compositions that can be employed to elicit an immune response or a protective immune response. In this aspect of the invention, an amount of a composition comprising recombinant DNA or mRNA encoding an polynucleotide of the subject invention sufficient to elicit an immune response or protective immune response is administered to an individual. Signal sequences may be deleted from the nucleic acid encoding an antigen of interest and the individual may be monitored for the induction of an immune response according to methods known in the art. A "protective immune response" or "therapeutic immune response" refers to a CTL (or $CD8^+$ T cell) and/or an HTL (or $CD4^+$ T cell) response to

an antigen that, in some way, prevents or at least partially arrests disease symptoms, side effects or progression. The immune response may also include an antibody response that has been facilitated by the stimulation of helper T cells.

[0042] In another embodiment, the subject invention further comprises the administration of polynucleotide vaccines in conjunction with a polypeptide antigen, or composition thereof, of the invention. In a preferred embodiment, the antigen is the polypeptide that is encoded by the polynucleotide administered as the polynucleotide vaccine. As a particularly preferred embodiment, the polypeptide antigen is administered as a booster subsequent to the initial administration of the polynucleotide vaccine.

[0043] A further embodiment of the subject invention provides for the induction of an immune response to the novel *Plasmodium falciparum* antigens disclosed herein (see, for example, the antigens and peptides set forth in the Tables and Sequence Listing attached hereto) using a "prime-boost" vaccination regimen known to those skilled in the art. In this aspect of the invention, a DNA vaccine is administered to an individual in an amount sufficient to "prime" the immune response of the individual, provided that the DNA vaccine comprises nucleic acids encoding the antigens, multi-epitope constructs, and/or peptide antigens set forth herein. The immune response of the individual is then "boosted" via the administration of: 1) one or a combination of: a peptide, polypeptide, and/or full length polypeptide antigen (*e.g.*, SEQ ID NOs: 1-27) of the subject invention (optionally in conjunction with a immunostimulatory molecule and/or an adjuvant); or 2) a viral vector that contains nucleic acid encoding one, or more, of the same or, optionally, different, antigens, multi-epitope constructs, and/or peptide antigens set forth in the Tables or Sequence Listing of the subject application. In some alternative embodiments of the invention, a gene encoding an immunostimulatory molecule may be incorporated into the viral vector used to "boost the immune response of the individual. Exemplary immunostimulatory molecules include, and are not limited to, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-15, Il-16, Il-18, IL-23, IL-24, erythropoietin, G-CSF, M-CSF, platelet derived growth factor (PDGF), MSF, FLT-3 ligand, EGF, fibroblast growth factor (FGF; *e.g.*, aFGF (FGF-1), bFGF (FGF-2), FGF-3, FGF-4, FGF-5, FGF-6, or FGF-7), insulin-like growth factors (*e.g.*, IGF-1, IGF-2); vascular endothelial growth factor (VEGF); interferons (*e.g.*, IFN-γ, IFN-α, IFN-β); leukemia inhibitory factor (LIF); ciliary neurotrophic factor (CNTF); oncostatin M; stem cell factor

(SCF); transforming growth factors (*e.g.*, TGF-α, TGF-β1, TGF-β1, TGF-β1), or chemokines (such as, but not limited to, BCA-1/BLC-1, BRAK/Kec, CXCL16, CXCR3, ENA-78/LIX, Eotaxin-1, Eotaxin-2/MPIF-2, Exodus-2/SLC, Fractalkine/Neurotactin, GROalpha/MGSA, HCC-1, I-TAC, Lymphotactin/ATAC/SCM, MCP-1/MCAF, MCP-3, MCP-4, MDC/STCP-1, ABCD-1, MIP-1α, MIP-1β, MIP-2α/GROβ, MIP-3α/Exodus/LARC, MIP-3β/Exodus-3/ELC, MIP-4/PARC/DC-CK1, PF-4, RANTES, SDF1α, TARC, or TECK). Genes encoding these immunostimulatory molecules are known to those skilled in the art and coding sequences may be obtained from a variety of sources, including various patents databases, publicly available databases (such as the nucleic acid and protein databases found at the National Library of Medicine or the European Molecular Biology Laboratory), the scientific literature, or scientific literature cited in catalogs produced by companies such as Genzyme, Inc., R&D Systems, Inc, or InvivoGen, Inc. [see, for example, the 1995 Cytokine Research Products catalog, Genzyme Diagnostics, Genzyme Corporation, Cambridge MA; 2002 or 1995 Catalog of R&D Systems, Inc (Minneapolis, MN); or 2002 Catalog of InvivoGen, Inc (San Diego, CA) each of which is incorporated by reference in its entirety, including all references cited therein].

[0044] Methods of introducing DNA vaccines into individuals are well-known to the skilled artisan. For example, DNA can be injected into skeletal muscle or other somatic tissues (e.g., intramuscular injection). Cationic liposomes or biolistic devices, such as a gene gun, can be used to deliver DNA vaccines. Alternatively, iontophoresis and other means for transdermal transmission can be used for the introduction of DNA vaccines into an individual.

[0045] Viral vectors for use in the subject invention can have a portion of the viral genome deleted to introduce new genes without destroying infectivity of the virus. The viral vector of the present invention is, typically, a non-pathogenic virus. At the option of the practitioner, the viral vector can be selected so as to infect a specific cell type, such as professional antigen presenting cells (*e.g.*, macrophage or dendritic cells). Alternatively, a viral vector can be selected that is able to infect any cell in the individual. Exemplary viral vectors suitable for use in the present invention include, but are not limited to poxvirus such as vaccinia virus, avipox virus, fowlpox virus, a highly attenuated vaccinia

virus (such as Ankara or MVA [Modified Vaccinia Ankara]), retrovirus, adenovirus, baculovirus and the like. In a preferred embodiment, the viral vector is Ankara or MVA.

[0046] General strategies for construction of vaccinia virus expression vectors are known in the art (see, for example, Smith and Moss Bio Techniques Nov/Dec, 306-312, 1984; U.S. Patent No. 4,738,846 (hereby incorporated by reference in its entirety). Sutter and Moss (Proc. Nat'l. Acad. Sci U.S.A. 89:10847-10851, 1992) and Sutter et al. (Vaccine, 12(11):1032-40, 1994) disclose the construction and use as a vector, a non-replicating recombinant Ankara virus (MVA) which can be used as a viral vector in the present invention. Other versions of the Modified Vaccinia Ankara strain can also be used in the practice of the subject invention (such as the MVA-BN strain produced by Bavarian Nordic S/A (Copenhagen, Denmark).

[0047] Compositions comprising the subject polynucleotides can include appropriate nucleic acid vaccine vectors (plasmids), which are commercially available (*e.g.*, Vical, San Diego, CA) or other nucleic acid vectors (plasmids), which are also commercially available (*e.g.*, Valenti, Burlingame, CA). Alternatively, compositions comprising viral vectors and polynucleotides according to the subject invention are provided by the subject invention. In addition, the compositions can include a pharmaceutically acceptable carrier, *e.g.*, saline. The pharmaceutically acceptable carriers are well known in the art and also are commercially available. For example, such acceptable carriers are described in E.W. Martin's *Remington's Pharmaceutical Science*, Mack Publishing Company, Easton, PA.

[0048] The subject invention also provides one or more isolated polypeptides comprising:

a) a polypeptide encoded by a polynucleotide sequence according to embodiment A(a) (set forth above);

b) a variant polypeptide encoded by a polynucleotide sequence having at least about 20% to 99.99% identity to a polynucleotide according to embodiment A(a) (as set forth above);

c) a fragment of a polypeptide or a variant polypeptide, wherein said fragment or variant has substantially the same serologic reactivity or substantially the same T-cell reactivity as the native polypeptide (*e.g.*, those polypeptides set

forth in SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27 and Table 2, 3, 4, 5 or 6);

d) a polypeptide sequence provided in Table 2, 3, 4, 5 or 6 or selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

e) a variant polypeptide having at least about 20% to 99.99% identity to a polypeptide provided in Table 2, 3, 4, 5 or 6 or selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27;

f) a polypeptide (epitope) set forth in Table 2, 3, 4, 5 or 6; or

g) a multi-epitope construct: 1) comprising at least one epitope set forth in Table 2, 3, 4, 5 or 6; 2) comprising a polypeptide selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27 and at least one epitope set forth in Tables 2, 3, 4, 5 or 6; or 3) comprising and at least one epitope set forth in Tables 2, 3, 4, 5 or 6 and one or more polypeptide selected from the group consisting of SEQ ID NO: NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27.

[0049] The term "peptide" may be used interchangeably with "oligopeptide" or "polypeptide" or "epitope" in the present specification to designate a series of residues, typically L-amino acids, connected one to the other, typically by peptide bonds between the α-amino and carboxyl groups of adjacent amino acids. The preferred CTL (or $CD8^+$ T cell)-inducing peptides of the invention are 13 residues or less in length and usually consist of between about 8 and about 11 residues (*e.g.*, 8, 9, 10 or 11 residues), preferably 9 or 10 residues. The preferred HTL (or $CD4^+$ T cell)-inducing peptides are less than about 50 residues in length and usually consist of between about 6 and about 30 residues, more usually between about 12 and 25 (*e.g.*, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25), and often between about 15 and 20 residues (*e.g.*, 15, 16, 17, 18, 19 or 20).

[0050] According to the subject invention, a "fragment" is a polypeptide of at least 3 consecutive, preferably 4 consecutive, and even more preferably 5 consecutive amino acids. In some embodiments, the polypeptide fragments are reactive with antibodies found in the serum of an individual. In other embodiments, a fragment is

an "epitope" as described *supra*. In the context of the instant invention, the terms polypeptide, peptide and protein can be used interchangeably; however, it should be understood that the invention does not relate to the polypeptides in natural form, that is to say that they are not in their natural environment but that the polypeptides may have been isolated or obtained by purification from natural sources, obtained from host cells prepared by genetic manipulation (*e.g.*, the polypeptides, or fragments thereof, are recombinantly produced by host cells, or by chemical synthesis). Polypeptides according to the instant invention may also contain non-natural amino acids, as will be described below.

[0051] A "variant" or "modified" polypeptide (or polypeptide variant) is to be understood to designate polypeptides exhibiting, in relation to the natural polypeptide, certain modifications. These modifications can include a deletion, addition, or substitution of at least one amino acid, a truncation, an extension, a chimeric fusion, a mutation, or polypeptides exhibiting post-translational modifications. Among the homologous polypeptides, those whose amino acid sequences exhibit between at least (or at least about) 20.00% to 99.99% (inclusive) identity to the full length, native, or naturally occurring polypeptide are another aspect of the invention. The aforementioned range of percent identity is to be taken as including, and providing written description and support for, any fractional percentage, in intervals of 0.01%, between 20.00% and, up to, including 99.99%. These percentages are purely statistical and differences between two polypeptide sequences can be distributed randomly and over the entire sequence length.

[0052] Variant peptides (epitopes) can also be created by altering the presence or absence of particular residues in these primary anchor positions. Such analogs are used to modulate the binding affinity of a peptide comprising a particular motif or supermotif. The term "motif" refers to the pattern of residues in a peptide of defined length, usually a peptide of from about 8 to about 13 amino acids for a class I HLA motif (*e.g.*, 8, 9, 10, 11, 12 or 13 aa) and from about 6 to about 25 amino acids for a class II HLA motif (*e.g.*, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 amino acids), which is recognized by a particular HLA molecule. Peptide motifs are typically different for each protein encoded by each human HLA allele and differ in the pattern of the primary and secondary anchor residues. Optionally, variant peptides or polypeptides can also comprise one or more heterologous polypeptide sequences (*e.g.*, tags that facilitate

purification of the polypeptides of the invention (see, for example, U.S. Patent No. 6,342,362, hereby incorporated by reference in its entirety; Altendorf *et al.* [1999-WWW, 2000] "Structure and Function of the F_o Complex of the ATP Synthase from *Escherichia Coli*," *J. of Experimental* Biology 203:19-28, The Co. of Biologists, Ltd., G.B.; Baneyx [1999] "Recombinant Protein Expression in *Escherichia coli*," Biotechnology 10:411-21, Elsevier Science Ltd.; Eihauer *et al.* [2001] "The FLAG™ Peptide, a Versatile Fusion Tag for the Purification of Recombinant Proteins," *J. Biochem Biophys Methods* 49:455-65; Jones *et al.* [1995] *J. Chromatography* 707:3-22; Jones *et al.* [1995] "Current Trends in Molecular Recognition and Bioseparation," *J. of Chromatography A.* 707:3-22, Elsevier Science B.V.; Margolin [2000] "Green Fluorescent Protein as a Reporter for Macromolecular Localization in Bacterial Cells," *Methods* 20:62-72, Academic Press; Puig *et al.* [2001] "The Tandem Affinity Purification (TAP) Method: A General Procedure of Protein Complex Purification," *Methods* 24:218-29, Academic Press; Sassenfeld [1990] "Engineering Proteins for Purification," TibTech 8:88-93; Sheibani [1999] "Prokaryotic Gene Fusion Expression Systems and Their Use in Structural and Functional Studies of Proteins," *Prep. Biochem. & Biotechnol.* 29(1):77-90, Marcel Dekker, Inc.; Skerra *et al.* [1999] "Applications of a Peptide Ligand for Streptavidin: the *Strep*-tag", *Biomolecular Engineering* 16:79-86, Elsevier Science, B.V.; Smith [1998] "Cookbook for Eukaryotic Protein Expression: Yeast, Insect, and Plant Expression Systems," *The* Scientist 12(22):20; Smyth *et al.* [2000] "Eukaryotic Expression and Purification of Recombinant Extracellular Matrix Proteins Carrying the Strep II Tag", *Methods in Molecular Biology*, 139:49-57; Unger [1997] "Show Me the Money: Prokaryotic Expression Vectors and Purification Systems," *The Scientist* 11(17):20, each of which is hereby incorporated by reference in their entireties), or commercially available tags from vendors such as such as STRATAGENE (La Jolla, CA), NOVAGEN (Madison, WI), QIAGEN, Inc., (Valencia, CA), or InVitrogen (San Diego, CA).

[0053] Variant polypeptides can, alternatively, have 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 percent identity with the polypeptide sequences of the instant invention. In a preferred embodiment, a variant or modified polypeptide exhibits approximately 85%, 86%, 87%,

88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to a natural polypeptic of the invention. Typically, the percent identity is calculated with reference to the full length, native, and/or naturally occurring polypeptide (*e.g.*, those polypeptides set forth in SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, or 27).

[0054] The nomenclature used to describe peptide compounds follows the conventional practice wherein the amino group is presented to the left (the N-terminus) and the carboxyl group to the right (the C-terminus) of each amino acid residue. When amino acid residue positions are referred to in an epitope, they are numbered in an amino to carboxyl direction with position one being the position closest to the amino terminal end of the epitope, or the peptide or protein of which it may be a part. In the formulae representing selected specific embodiments of the present invention, the amino- and carboxyl-terminal groups, although not specifically shown, are in the form they would assume at physiologic pH values, unless otherwise specified. In the amino acid structure formulae, each residue is generally represented by standard three-letter or single-letter designations (*e.g.*, as set forth *infra)*. By way of example, amino acid substitutions can be carried out without resulting in a substantial modification of the biological activity of the corresponding modified polypeptides; for example, the replacement of leucine with valine or isoleucine, of aspartic acid with glutamic acid, of glutamine with asparagine, of arginine with lysine, and the like, the reverse substitutions can be performed without substantial modification of the biological activity of the polypeptides.

[0055] The L-form of an amino acid residue is represented by a capital single letter or a capital first letter of a three-letter symbol, and the D-form, for those amino acids having D-forms, is represented by a lower case single letter or a lower case three letter symbol. Glycine has no asymmetric carbon atom and is simply referred to as "Gly" or G. Symbols for the amino acids are as follows: (Single Letter Symbol; Three Letter Symbol Amino Acid) A; Ala; Alanine: C; Cys; Cysteine: D; Asp; Aspartic Acid: E; Glu; Glutamic Acid: F; Phe; Phenylalanine: G; Gly; Glycine: H; His; Histidine: I; Ile; Isoleucine: K; Lys; Lysine: L; Leu; Leucine: M; Met; Methionine: N; Asn; Asparagine: P; Pro; Proline: Q; Gln; Glutamine: R; Arg; Arginine: S; Ser; Serine: T; Thr; Threonine: V; Val; Valine: W; Trp; Tryptophan: Y; Tyr; Tyrosine.

[0056] Amino acid "chemical characteristics" are defined as: Aromatic (F, W, Y); Aliphatic-hydrophobic (L, I, V, M); Small polar (S, T, C); Large polar (Q, N); Acidic (D, E); Basic (R, H, K); Non-polar: Proline; Alanine; and Glycine.

[0057] In order to extend the life of the polypeptides according to the invention, it may be advantageous to use non-natural amino acids, for example in the D-form, or alternatively amino acid analogs, for example sulfur-containing forms of amino acids in the production of "variant polypeptides". Alternative means for increasing the life of polypeptides can also be used in the practice of the instant invention. For example, polypeptides of the invention, and fragments thereof, can be recombinantly modified to include elements that increase the plasma, or serum half-life of the polypeptides of the invention. These elements include, and are not limited to, antibody constant regions (see for example, U.S. Patent No. 5,565,335, hereby incorporated by reference in its entirety, including all references cited therein), or other elements such as those disclosed in U.S. Patent Nos. 6,319,691, 6,277,375, or 5,643,570, each of which is incorporated by reference in its entirety, including all references cited within each respective patent. Alternatively, the polynucleotides and genes of the instant invention can be recombinantly fused to elements, well known to the skilled artisan, that are useful in the preparation of immunogenic constructs for the purposes of vaccine formulation.

[0058] The subject invention also provides biologically active fragments (epitopes) of a polypeptide according to the invention and includes those peptides capable of eliciting an immune response directed against *P. falciparum*, said immune response providing components (B-cells, antibodies, and/or or components of the cellular immune response (*e.g.*, helper, cytotoxic, and/or suppressor T-cells)) reactive with the biologically active fragment of a polypeptide; the intact, full length, unmodified polypeptide disclosed herein; or both the biologically active fragment of a polypeptide and the intact, full length, unmodified polypeptides disclosed herein.

[0059] Fragments, as described herein, can be obtained by cleaving the polypeptides of the invention with a proteolytic enzyme (such as trypsin, chymotrypsin, or collagenase) or with a chemical reagent, such as cyanogen bromide (CNBr). Alternatively, polypeptide fragments can be generated in a highly acidic environment, for example at pH 2.5. Such polypeptide fragments may be equally well prepared by chemical synthesis or using hosts transformed with an expression vector according to the

invention. The transformed host cells contain a nucleic acid, allowing the expression of these fragments, under the control of appropriate elements for regulation and/or expression of the polypeptide fragments.

[0060] In one embodiment, the subject invention provides methods for eliciting an immune response in an individual comprising the administration of compositions comprising polypeptides according to the subject invention to an individual in amounts sufficient to induce an immune response in the individual. In some embodiments, a "protective" or "therapeutic immune response" is induced in the individual. A "protective immune response" or "therapeutic immune response" refers to a CTL (or $CD8^+$ T cell) and/or an HTL (or $CD4^+$ T cell), and/or an antibody response to an antigen derived from an infectious agent or a tumor antigen, which in some way prevents or at least partially arrests disease symptoms, side effects or progression. The protective immune response may also include an antibody response that has been facilitated by the stimulation of helper T cells (or $CD4^+$ T cells). Additional methods of inducing an immune response in an individual are taught in U.S. Patent No. 6,419,931, hereby incorporated by reference in its entirety. The term CTL can be used interchangeably with $CD8^+$ T-cell(s) and the term HTL can be used interchangeably with $CD4^+$ T-cell(s) throughout the subject application.

[0061] The term "individual" includes mammals which include, and are not limited to, apes, chimpanzees, orangutans, humans, monkeys or domesticated animals (pets) such as dogs, cats, guinea pigs, hamsters, Vietnamese pot-bellied pigs, rabbits, ferrets, cows, horses, goats and sheep. In a preferred embodiment, the methods of inducing an immune response contemplated herein are practiced on humans.

[0062] Another embodiment of the subject invention provides methods of inducing an immune response in an individual comprising the administration of a composition comprising polypeptides encoded by the polynucleotides of the subject invention in amounts sufficient to induce an immune response. In some embodiments of the invention, the immune response provides protective immunity. The composition administered to the individual may, optionally, contain an adjuvant and may be delivered in any manner known in the art for the delivery of immunogen to a subject. Compositions may also be formulated in any carriers, including for example, pharmaceutically acceptable carriers such as those described in E.W. Martin's

Remington's Pharmaceutical Science, Mack Publishing Company, Easton, PA. In a preferred embodiment, compositions may be formulated in incomplete Freund's adjuvant.

[0063] In various embodiments, the subject invention provides for diagnostic assays based upon Western blot formats or standard immunoassays known to the skilled artisan. For example, antibody-based assays such as enzyme linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), lateral flow assays, immunochromatographic strip assays, automated flow assays, and assays utilizing antibody-containing biosensors may be employed for the detection of the polypeptides, and fragments thereof, provided by the subject invention. The assays and methods for conducting the assays are well-known in the art and the methods may test biological samples qualitatively (presence or absence of polypeptide) or quantitatively (comparison of a sample against a standard curve prepared using a polypeptide of the subject invention) for the presence of one or more polypeptide of the subject invention. Thus, the subject invention provides a method of detecting a *P. falciparum* polypeptide, or fragment thereof, comprising contacting a sample with an antibody that specifically binds to a polypeptide, or fragment thereof, comprising SEQ ID NOs: 1-26, or 27 and detecting the presence of an antibody-antigen complex.

[0064] The antibody-based assays can be considered to be of four types: direct binding assays, sandwich assays, competition assays, and displacement assays. In a direct binding assay, either the antibody or antigen is labeled, and there is a means of measuring the number of complexes formed. In a sandwich assay, the formation of a complex of at least three components (*e.g.*, antibody-antigen-antibody) is measured. In a competition assay, labeled antigen and unlabelled antigen compete for binding to the antibody, and either the bound or the free component is measured. In a displacement assay, the labeled antigen is pre-bound to the antibody, and a change in signal is measured as the unlabelled antigen displaces the bound, labeled antigen from the receptor.

[0065] Lateral flow assays can be conducted according to the teachings of U.S. Patent No. 5,712,170 and the references cited therein. U.S. Patent No. 5,712,170 and the references cited therein are hereby incorporated by reference in their entireties. Displacement assays and flow immunosensors useful for carrying out displacement assays are described in: (1) Kusterbeck *et al.*, "Antibody-Based Biosensor for Continuous Monitoring", in Biosensor Technology, R. P. Buck *et al.*, eds., Marcel Dekker, N.Y. pp.

345-350 (1990); Kusterbeck *et al.*, "A Continuous Flow Immunoassay for Rapid and Sensitive Detection of Small Molecules", Journal of Immunological Methods, vol. 135, pp. 191-197 (1990); Ligler *et al.*, "Drug Detection Using the Flow Immunosensor", in Biosensor Design and Application, J. Findley *et al.*, eds., American Chemical Society Press, pp. 73-80 (1992); and Ogert *et al.*, "Detection of Cocaine Using the Flow Immunosensor", Analytical Letters, vol. 25, pp. 1999-2019 (1992), all of which are incorporated herein by reference in their entireties. Displacement assays and flow immunosensors are also described in U.S. Patent No. 5,183,740, which is also incorporated herein by reference in its entirety. The displacement immunoassay, unlike most of the competitive immunoassays used to detect small molecules, can generate a positive signal with increasing antigen concentration. One aspect of the invention allows for the exclusion of Western blots as a diagnostic assay, particularly where the Western blot is a screen of whole cell lysates of *P. falciparum*, or related organisms, against immune serum of infected individuals. In another aspect of the invention, peptide, or polypeptide, based diagnostic assays utilize *P. falciparum* peptides or polypeptides that have been produce either by chemical peptide synthesis or by recombinant methodologies that utilize non-plasmodium host cells for the production of peptides or polypeptides.

[0066] Another aspect of the invention provides for the use of peptides, polypeptides, and multi-epitope constructs in assays such as those taught in U.S. Patent No. 5,635,363, which is hereby incorporated by reference in its entirety. Briefly, peptides, polypeptides, and multi-epitope constructs of the subject invention can be used to form stable multimeric complexes that comprise prepared major histocompatibility complex (MHC) protein subunits having a substantially homogeneous bound peptide population. The multimeric MHC-antigen complex forms a stable structure with T cells recognizing the complex through their antigen receptor, thereby allowing for the labeling, identification and separation of specific T cells. The multimeric binding complex has the formula $(\alpha\text{-}\beta\text{-}P)_n$, where $n \geq 2$, usually $n \geq 4$, and usually $n \leq 10$; α is an α chain of a class I or class II MHC protein. β is a β chain, (the β chain of a class II MHC protein or β_2 microglobulin for a MHC class I protein; and P is a peptide antigen. The multimeric complex stably binds through non-covalent interactions to a T cell receptor having the appropriate antigenic specificity. The MHC proteins may be from any individual. Of particular interest are the human HLA proteins. Included in the HLA proteins are the

class II subunits HLA-DPα, HLA-DPβ, HLA-DQα, HLA-DQβ, HLA-DRα and HLA-DRβ, and the class I proteins HLA-A, HLA-B, HLA-C, and β_2 -microglobulin. In a preferred embodiment, the MHC protein subunits are a soluble form of the normally membrane-bound protein. The soluble form is derived from the native form by deletion of the transmembrane domain. Conveniently, the protein is truncated, removing both the cytoplasmic and transmembrane domains. The protein may be truncated by proteolytic cleavage, or by expressing a genetically engineered truncated form. For class I proteins, the soluble form will include the α1, α2 and α3 domain. Not more than about 10, usually not more than about 5, preferably none of the amino acids of the transmembrane domain will be included. The deletion may extend as much as about 10 amino acids into the α3 domain, preferably none of the amino acids of the α3 domain will be deleted. The deletion will be such that it does not interfere with the ability of the α3 domain to fold into a disulfide bonded structure. The class I β chain, β_2-microglobulin, lacks a transmembrane domain in its native form, and need not be truncated. Generally, no Class II subunits will be used in conjunction with Class I subunits. Soluble class II subunits will include the α1 and α2 domains for the α subunit, and the β1 and β2 domains for the β subunit. Not more than about 10, usually not more than about 5, preferably none of the amino acids of the transmembrane domain will be included. The deletion may extend as much as about 10 amino acids into the α2 or β2 domain, preferably none of the amino acids of the β2 or β2 domain will be deleted. The deletion will be such that it does not interfere with the ability of the α2 or β2 domain to fold into a disulfide bonded structure.

[0067] The monomeric complex (α-β-P) (monomer) is multimerized. The resulting multimer will be stable over long periods of time. Usually not more than about 10% of the multimer will be dissociated after storage at 4° C for about one day, more usually after about one week. Preferably, the multimer will be formed by binding the monomers to a multivalent entity through specific attachment sites on the α or β subunit, as described below in detail. The multimer may also be formed by chemical cross-linking of the monomers. A number of reagents capable of cross-linking proteins are known in the art, illustrative entities include: azidobenzoyl hydrazide, N-[4-(p-azidosalicylamino)butyl]-3'-[2'-pyridyldithio]propionamide), bis-sulfosuccinimidyl suberate, dimethyladipimidate, disuccinimidyltartrate, N-.gamma.-maleimidobutyryloxysuccinimide ester, N-hydroxy sulfosuccinimidyl-4-azidobenzoate,

N-succinimidyl [4-azidophenyl]-1,3'-dithiopropionate, N-succinimidyl [4-iodoacetyl]aminobenzoate, glutaraldehyde, formaldehyde and succinimidyl 4-[N-maleimidomethyl]cyclohexane-1-carboxylate.

[0068] The attachment site for binding to a multivalent entity may be naturally occurring, or may be introduced through genetic engineering. The site will be a specific binding pair member or one that is modified to provide a specific binding pair member, where the complementary pair has a multiplicity of specific binding sites. Binding to the complementary binding member can be a chemical reaction, epitope-receptor binding or hapten-receptor binding where a hapten is linked to the subunit chain. In a preferred embodiment, one of the subunits is fused to an amino acid sequence providing a recognition site for a modifying enzyme. The recognition sequence will usually be fused proximal to the carboxy terminus of one of the subunit to avoid potential hindrance at the antigenic peptide binding site. Conveniently, an expression cassette will include the sequence encoding the recognition site.

[0069] Modifying enzymes of interest include BirA, various glycosylases, farnesyl protein transferase, protein kinases and the like. The subunit may be reacted with the modifying enzyme at any convenient time, usually after formation of the monomer. The group introduced by the modifying enzyme, e.g. biotin, sugar, phosphate, farnesyl, etc. provides a complementary binding pair member, or a unique site for further modification, such as chemical cross-linking, biotinylation, etc. that will provide a complementary binding pair member. An alternative strategy is to introduce an unpaired cysteine residue to the subunit, thereby introducing a unique and chemically reactive site for binding. The attachment site may also be a naturally occurring or introduced epitope, where the multivalent binding partner will be an antibody, e.g. IgG, IgM, etc. Any modification will be at a site, e.g. C-terminal proximal, that will not interfere with binding.

[0070] Exemplary of multimer formation is the introduction of the recognition sequence for the enzyme BirA, which catalyzes biotinylation of the protein substrate. The monomer with a biotinylated subunit is then bound to a multivalent binding partner, e.g. streptavidin or avidin, to which biotin binds with extremely high affinity. Streptavidin has a valency of 4, providing a multimer of $(\alpha\text{-}\beta\text{-}P)_4$.

[0071] The multivalent binding partner may be free in solution, or may be attached to an insoluble support. Examples of suitable insoluble supports include beads, e.g. magnetic beads, membranes and microtiter plates. These are typically made of glass, plastic (e.g. polystyrene), polysaccharides, nylon or nitrocellulose. Attachment to an insoluble support is useful when the binding complex is to be used for separation of T cells.

[0072] Frequently, the multimeric complex will be labeled, so as to be directly detectable, or will be used in conjunction with secondary labeled immunoreagents which will specifically bind the complex. In general the label will have a light detectable characteristic. Preferred labels are fluorophors, such as fluorescein isothiocyanate (FITC), rhodamine, Texas Red, phycoerythrin and allophycocyanin. Other labels of interest may include dyes, enzymes, chemiluminescers, particles, radioisotopes, or other directly or indirectly detectable agent. Conveniently, the multivalent binding partner will have the labeling group. Alternatively, a second stage label may be used, e.g. labeled antibody directed to one of the peptide constituents, and the like.

[0073] The binding complex will be used to detect and/or separate antigen specific T cells. The T cells may be from any source, usually having the same species of origin as the MHC heterodimer. The T cells may be from an in vitro culture, or a physiologic sample. For the most part, the physiologic samples employed will be blood or lymph, but samples may also involve other sources oft cells, particularly where T cells may be invasive. Thus other sites of interest are tissues, or associated fluids, as in the brain, lymph node, neoplasms, spleen, liver, kidney, pancreas, tonsil, thymus, joints, synovia, and the like. The sample may be used as obtained or may be subject to modification, as in the case of dilution, concentration, or the like. Prior treatments may involve removal of cells by various techniques, including centrifugation, using Ficoll-Hypaque, panning, affinity separation, using antibodies specific for one or more markers present as surface membrane proteins on the surface of cells, or any other technique that provides enrichment of the set or subset of cells of interest.

[0074] The binding complex is added to a suspension comprising T cells of interest, and incubated at about 4° C for a period of time sufficient to bind the available cell surface receptor. The incubation will usually be at least about 5 minutes and usually

less than about 30 minutes. It is desirable to have a sufficient concentration of labeling reagent in the reaction mixture, so that labeling reaction is not limited by lack of labeling reagent. The appropriate concentration is determined by titration. The medium in which the cells are labeled will be any suitable medium as known in the art. If live cells are desired a medium will be chosen that maintains the viability of the cells. A preferred medium is phosphate buffered saline containing from 0.1 to 0.5% BSA. Various media are commercially available and may be used according to the nature of the cells, including Dulbecco's Modified Eagle Medium (dMEM), Hank's Basic Salt Solution (HBSS), Dulbecco's phosphate buffered saline (dPBS), RPMI, Iscove's medium, PBS with 5 mM EDTA, etc., frequently supplemented with fetal calf serum, BSA, HSA, etc.

[0075] Where a second stage labeling reagent is used, the cell suspension may be washed and resuspended in medium as described above prior to incubation with the second stage reagent. Alternatively, the second stage reagent may be added directly into the reaction mix.

[0076] A number of methods for detection and quantitation of labeled cells are known in the art. Flow cytometry is a convenient means of enumerating cells that are a small percent of the total population. Fluorescent microscopy may also be used. Various immunoassays, e.g. ELISA, RIA, etc. may used to quantitate the number of cells present after binding to an insoluble support.

[0077] Flow cyometry may also be used for the separation of a labeled subset of T cells from a complex mixture of cells. The cells may be collected in any appropriate medium which maintains the viability of the cells, usually having a cushion of serum at the bottom of the collection tube. Various media are commercially available as described above. The cells may then be used as appropriate.

[0078] Alternative means of separation utilize the binding complex bound directly or indirectly to an insoluble support, e.g. column, microtiter plate, magnetic beads, etc. The cell sample is added to the binding complex. The complex may be bound to the support by any convenient means. After incubation, the insoluble support is washed to remove non-bound components. From one to six washes may be employed, with sufficient volume to thoroughly wash non-specifically bound cells present in the sample. The desired cells are then eluted from the binding complex. In particular the use of

magnetic particles to separate cell subsets from complex mixtures is described in Miltenyi et al. (1990) Cytometry 11:231-238.

[0079] Detecting and/or quantitating specific T cells in a sample or fraction thereof may be accomplished by a variety of specific assays. In general, the assay will measure the binding between a patient sample, usually blood derived, generally in the form of plasma or serum and the subject multimeric binding complexes. The patient sample may be used directly, or diluted as appropriate, usually about 1:10 and usually not more than about 1:10,000. Assays may be performed in any physiological buffer, e.g. PBS, normal saline, HBSS, dPBS, etc.

[0080] A sandwich assay is performed by first attaching the multimeric binding complex to an insoluble surface or support. The multimeric binding complex may be bound to the surface by any convenient means, depending upon the nature of the surface, either directly or through specific antibodies. The particular manner of binding is not crucial so long as it is compatible with the reagents and overall methods of the invention. They may be bound to the plates covalently or non-covalently, preferably non-covalently.

[0081] The insoluble supports may be any compositions to which the multimeric binding complex can be bound, which is readily separated from soluble material, and which is otherwise compatible with the overall method of measuring T cells. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports to which the receptor is bound include beads, e.g. magnetic beads, membranes and microtiter plates. These are typically made of glass, plastic (e.g. polystyrene), polysaccharides, nylon or nitrocellulose. Microtiter plates are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples.

[0082] Before adding patient samples or fractions thereof, the non-specific binding sites on the insoluble support i.e. those not occupied by the multimeric binding complex, are generally blocked. Preferred blocking agents include non-interfering proteins such as bovine serum albumin, casein, gelatin, and the like. Samples, fractions or aliquots thereof are then added to separately assayable supports (for example, separate wells of a microtiter plate) containing support-bound multimeric binding complex.

[0083] Generally from about 0.001 to 1 ml of sample, diluted or otherwise, is sufficient, usually about 0.01 ml sufficing. Preferably, each sample and standard will be added to multiple wells so that mean values can be obtained for each. The incubation time should be sufficient for T cells to bind the insoluble binding complex. Generally, from about 0.1 to 3 hr is sufficient, usually 1 hr sufficing.

[0084] After incubation, the insoluble support is generally washed of non-bound components. Generally, a dilute physiologic buffer at an appropriate pH, generally 7-8, is used as a wash medium. From one to six washes may be employed, with sufficient volume to thoroughly wash non-specifically bound T cells present in the sample.

[0085] After washing, a solution containing specific second receptor is applied. The receptor may be any compound that binds patient T cells with sufficient specificity such that they can be distinguished from other components present. In a preferred embodiment, second receptors are antibodies specific for common T cell antigens, either monoclonal or polyclonal sera, e.g. anti-thy-1, anti-CD45, etc.

[0086] T cell specific antibodies may be labeled to facilitate direct or indirect quantification of binding. Examples of labels that permit direct measurement include radiolabels, such as ^{3}H or ^{125}I, fluorescers, dyes, beads, chemilumninescers, colloidal particles, and the like. Examples of labels which permit indirect measurement of binding include enzymes where the substrate may provide for a colored or fluorescent product. Examples of suitable enzymes for use in conjugates include horseradish peroxidase, alkaline phosphatase, malate dehydrogenase and the like. Where not commercially available, such antibody-enzyme conjugates are readily produced by techniques known to those skilled in the art.

[0087] Alternatively, the second receptor may be unlabeled. In this case, a labeled second receptor-specific compound is employed which binds to the bound second receptor. Such a second receptor-specific compound can be labelled in any of the above manners. It is possible to select such compounds such that multiple compounds bind each molecule of bound second receptor. Examples of second receptor/second receptor-specific molecule pairs include antibody/anti-antibody and avidin (or streptavidin)/biotin. Since the resultant signal is thus amplified, this technique may be advantageous where only a small number oft cells are present. An example is the use of a labeled antibody

specific to the second receptor. More specifically, where the second receptor is a rabbit anti-allotypic antibody, an antibody directed against the constant region of rabbit antibodies provides a suitable second receptor specific molecule. The anti-immunoglobulin will usually come from any source other than human, such as ovine, rodentia, particularly mouse, or bovine.

[0088] The volume, composition and concentration of T cell specific receptor solution provides for measurable binding to the T cells already bound to the insoluble substrate. Generally, the same volume as that of the sample is used: from about 0.001 to 1 ml is sufficient, usually about 0.1 ml sufficing. When antibody ligands are used, the concentration generally will be about 0.1 to 50 μg/ml, preferably about 1 μg/ml. The solution containing the second receptor is generally buffered in the range of about pH 6.5-9.5. The solution may also contain an innocuous protein as previously described. The incubation time should be sufficient for the labeled ligand to bind available molecules. Generally, from about 0.1 to 3 hr is sufficient, usually 1 hr sufficing.

[0089] After the second receptor or second receptor-conjugate has bound, the insoluble support is generally again washed free of non-specifically bound second receptor, essentially as described for prior washes. After non-specifically bound material has been cleared, the signal produced by the bound conjugate is detected by conventional means. Where an enzyme conjugate is used, an appropriate enzyme substrate is provided so a detectable product is formed. More specifically, where a peroxidase is the selected enzyme conjugate, a preferred substrate combination is H_2O_2 and O-phenylenediamine which yields a colored product under appropriate reaction conditions. Appropriate substrates for other enzyme conjugates such as those disclosed above are known to those skilled in the art. Suitable reaction conditions as well as means for detecting the various useful conjugates or their products are also known to those skilled in the art. For the product of the substrate O-phenylenediamine for example, light absorbance at 490-495 nm is conveniently measured with a spectrophotometer.

[0090] Generally the number of bound T cells detected will be compared to control samples from samples having a different MHC context, e.g. T cells from an animal that does not express the MHC molecule used to make the binding complex.

[0091] An alternative protocol is to provide anti-T cell reagent, e.g. anti-thy-1, anti-CD45, etc. bound to the insoluble surface. After adding the sample and washing away non-specifically bound T cells, one or a combination of the subject binding complexes are added, where the binding complexes are labeled so as not to interfere with the binding to T cells.

[0092] It is particularly convenient in a clinical setting to perform the assays in a self-contained apparatus. A number of such methods are known in the art. The apparatus will generally employ a continuous flow-path of a suitable filter or membrane, having at least three regions, a fluid transport region, a sample region, and a measuring region. The sample region is prevented from fluid transfer contact with the other portions of the flow path prior to receiving the sample. After the sample region receives the sample, it is brought into fluid transfer relationship with the other regions, and the fluid transfer region contacted with fluid to permit a reagent solution to pass through the sample region and into the measuring region. The measuring region may have bound to it the multimeric binding complex, with a conjugate of an enzyme with T cell specific antibody employed as a reagent, generally added to the sample before application. Alternatively, the binding complex may be conjugated to an enzyme, with T cell specific antibody bound to the measurement region.

[0093] Detection of T cells is of interest in connection with a variety of conditions associated with T cell activation. Such conditions include autoimmune diseases, e.g. multiple sclerosis, myasthenia gravis, rheumatoid arthritis, type 1 diabetes, graft vs. host disease, Grave's disease, etc.; various forms of cancer, e.g. carcinomas, melanomas, sarcomas, lymphomas and leukemias. Various infectious diseases such as those caused by viruses, e.g. HIV-1, hepatitis, herpesviruses, enteric viruses, respiratory viruses, rhabdovirus, rubeola, poxvirus, paramyxovirus, morbillivirus, etc. are of interest. Infectious agents of interest also include bacteria, such as Pneumococcus, Staphylococcus, Bacillus. Streptococcus, Meningococcus, Gonococcus, Eschericia, Klebsiella, Proteus, Pseudomonas, Salmonella, Shigella, Hemophilus, Yersinia, Listeria, Corynebacterium, Vibrio, Clostridia, Chlamydia, Mycobacterium, Helicobacter and Treponema; protozoan pathogens, and the like. T cell associated allergic responses may also be monitored, e.g. delayed type hypersensitivity or contact hypersensitivity involving T cells.

[0094] Of particular interest are conditions having an association with a specific peptide or MHC haplotype, where the subject binding complexes may be used to track the T cell response with respect to the haplotype and antigen. A large number of associations have been made in disease states that suggest that specific MHC haplotypes, or specific protein antigens are responsible for disease states.

[0095] Polypeptide fragments, including immunogenic fragments, for each of SEQ ID NOs: 1-27 can be any length from at least 5 consecutive amino acids to 1 amino acid less than a full length polypeptide of any given SEQ ID NO:. Thus, for SEQ ID NO: 1 (used here as a non-limiting example) the polypeptide fragment can contain any number of consecutive amino acids from 5 to 1903 (for example, 5, 6, 7, ... , 1901, 1902, 1903). For the sake of brevity, the individual integers between 5 and 1903 have not been reproduced herein but are, in fact, specifically contemplated. In one embodiment, the immunogenic fragments of the invention induce immunity or protective immunity from disease.

[0096] The present invention also provides for the exclusion of any individual fragment (of any given SEQ ID NO:) specified by N-terminal to C-terminal positions, actual sequence, or of any fragment specified by size (in amino acid residues) as described above. In addition, any number of fragments specified by N-terminal and C-terminal positions, actual sequence, or by size (in amino acid residues) as described above may be excluded as individual species. Further, any number of fragments specified by N-terminal and C-terminal positions or by size (in amino acid residues) as described above may be combined to provide a polypeptide fragment. These types of fragments may, optionally, include polypeptide sequences such as linkers, described below.

[0097] Where a claim recites "a polypeptide comprising SEQ ID NO: X, or fragments or immunogenic fragments or epitopes of SEQ ID NO:X", the language "fragments or immunogenic fragments or epitopes of SEQ ID NO:X" specifically excludes identical sub-sequences found within other longer naturally occurring prior art polypeptide or protein sequences that are not identical to sequence from which the claimed sequence was derived. This does not include instances where such sub-sequences are a part of a larger molecule specifically modified by the hand of man to enhance the immunogenicity of the fragments of the subject invention. Thus, fragments or immunogenic fragments or epitopes of SEQ ID NO:X specifically exclude, and are not

to be considered anticipated, where the fragment is a sub-sequence of another naturally occurring non-malarial peptide, polypeptide, or protein isolated from a bacterial, viral, reptilian, insect, avian, or mammalian source and is identified in a search of protein sequence databases.

[0098] Fragments or immunogenic fragments or epitopes of the invention may further contain linkers that facilitate the attachment of the fragments to a carrier molecule for the stimulation of an immune response or diagnostic purposes. The linkers can also be used to attach fragments according to the invention to solid support matrices for use in affinity purification protocols. In this aspect of the invention, the linkers specifically exclude, and are not to be considered anticipated, where the fragment is a subsequence of another peptide, polypeptide, or protein as identified in a search of protein sequence databases as indicated in the preceding paragraph. In other words, the non-identical portions of the other peptide, polypeptide, of protein are not considered to be a "linker" in this aspect of the invention. Non-limiting examples of "linkers" suitable for the practice of the invention include chemical linkers (such as those sold by Pierce, Rockford, IL) and peptides that allow for the connection of the immunogenic fragment to a carrier molecule (see, for example, linkers disclosed in U.S. Patent Nos. 6,121,424, 5,843,464, 5,750,352, and 5,990,275, hereby incorporated by reference in their entirety). In various embodiments, the linkers can be up to 50 amino acids in length, up to 40 amino acids in length, up to 30 amino acids in length, up to 20 amino acids in length, up to 10 amino acids in length, or up to 5 amino acids in length. Of course, the linker may be any pre-selected number of amino acids (up to 50 amino acids) in length.

[0099] In various embodiments, polypeptides suitable for use in various disclosed methods of the subject invention can be selected from the group consisting of: a) a polypeptide comprising a polypeptide sequence selected from the group consisting of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16 ,17, 18, 19, 20, 21 ,22, 23, 24, 25, 26, and 27; b) a variant polypeptide having at least about 20% to 99.99% identity to a polypeptide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16 ,17, 18, 19, 20, 21 ,22, 23, 24, 25, 26, and 27; c) a fragment of a polypeptide or a variant polypeptide of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16 ,17, 18, 19, 20, 21 ,22, 23, 24, 25, 26, or 27, wherein said fragment or variant

has substantially the same serologic reactivity or substantially the same T-cell reactivity as the native polypeptide; d) a multi-epitope construct; and e) combinations thereof.

Multi-epitope constructs

[00100] As indicated *supra*, the subject invention provides for "multi-epitope constructs". A "multi-epitope construct" comprises: 1) nucleic acids that encode multiple polypeptide epitopes (of any length) that can bind to one or more molecules functioning in the immune system; or 2) polypeptides comprising multiple polypeptide epitopes that can bind to one or more molecules functioning in the immune system. "Multi-epitope constructs" can, optionally, contain "flanking" or "spacing" residues between each epitope. Some embodiments provide for "multi-epitope constructs" that comprise a series of the same epitope (termed "homopolymers"). Other embodiments provide for "multi-epitope constructs" that comprise a combination or series of different epitopes, optionally connected by "flanking" or "spacing" residues (termed "heteropolymers"). In some embodiments, "multi-epitope constructs" may exclude full-length polypeptides from which the epitopes are obtained (*e.g.*, the polypeptides of SEQ ID NOs: 1-27). In certain preferred embodiments, the epitopes used in the formation of the multi-epitope construct are selected from those set forth in Table 2, Table 3, Table 4, Table 5, and/or Table 6 and any epitope set forth in these Tables 2-6 can be mixed and/or matched any other epitope set forth in any of the aforementioned Tables 2-6.

[00101] Multi-epitope constructs may be of "high affinity" or "intermediate affinity". As used herein, "high affinity" with respect to HLA class I molecules is defined as binding with an IC_{50}, or KD value, of 50 nM or less; "intermediate affinity" with respect to HLA class I molecules is defined as binding with an IC_{50} or KD value of between about 50 and about 500 nM. "High affinity" with respect to binding to HLA class II molecules is defined as binding with an IC_{50} or KD value of 100 nM or less; "intermediate affinity" with respect to binding to HLA class II molecules is defined as binding with an IC_{50} or KD value of between about 100 and about 1000 nM.

[00102] The multi-epitope constructs described herein preferably include five or more, ten or more, fifteen or more, twenty or more, or twenty-five or more epitopes. Other embodiments provide multi-epitope constructs that comprise at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33,

34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 epitopes. All of the epitopes in a multi-epitope construct may be from one organism (*e.g.*, the epitopes are obtained from *P. falciparum*), or the multi-epitope construct may include epitopes present in two or more different organisms (*e.g.*, some epitopes from *P. falciparum* and some epitopes from another organism). Additionally, the same epitope may be present in a multi-epitope construct at more than one location in the construct. In some embodiments, novel epitopes of the subject invention may be linked to known epitopes of an organism (*e.g., P. falciparum* or another organism).

[00103] A "multi-epitope vaccine," is a vaccine comprising multiple epitopes. A multi-epitope vaccine can induce an immune response and is administered to an individual in an amount sufficient to induce an immune response in the individual. In some embodiments, the immune response induced by the multi-epitope vaccine is a protective immune response against a given organism, pathogen, or pathologic condition (*e.g., P. falciparum*).

[00104] In certain embodiments, the epitopes of a multi-epitope construct or the polypeptides disclosed herein interact with an antigen binding site of an antibody molecule, a class I HLA, a T-cell receptor, and/or a class II HLA molecule. In certain preferred embodiments, the epitopes interact with an HLA molecule (*e.g.*, class I or class II) or a T-cell receptor. In an even more preferred embodiment, the epitope interacts with both an HLA molecule (*e.g.*, class I or class II) and a T-cell receptor. In various embodiments, all of the nucleic acids in a multi-epitope construct can encode class I HLA epitopes or class II HLA epitopes. Multi-epitope constructs comprising epitopes that interact exclusively with class I HLA molecules may be referred to as "CTL multi-epitope constructs" (or "$CD8^+$ T cell multi-epitope constructs"). Multi-epitope constructs comprising epitopes that interact exclusively with class II HLA molecules may be referred to as "HTL multi-epitope constructs" (or "$CD4^+$ T cell multi epitope constructs"). Some multi-epitope constructs (designated "TL multi-epitope constructs") can have a subset of the multi-epitope nucleic acids encoding class I HLA epitopes and another subset of the multi-epitope nucleic acids encoding class II HLA epitopes (*e.g.*, the constructs stimulate both CTL (*i.e.*, $CD8^+$ T cell) and HTL (*i.e.*, $CD4^+$ T cell) of the

immune system). Other multi-epitope constructs can provide epitopes that interact exclusively with B-cells or immunoglobulin molecules and are designated "BL multi-epitope constructs". Multi-epitope constructs that provide epitopes that interact with B-cells (and/or immunoglobulin molecules) and further provide class I HLA epitopes and class II HLA epitopes are designated "immune system (IMS) multi-epitope constructs". In certain embodiments, multi-epitope constructs can provide class I or class II epitopes (*e.g.*, CTL (*i.e.*, $CD8^+$ T cell) epitopes or HTL (*i.e.*, $CD4^+$ T cell) epitopes) and BL epitopes. "Human Leukocyte Antigen" or "HLA" is a human class I or class II Major Histocompatibility Complex (MHC) protein (see, *e.g.*, Stites, *et al.*, IMMUNOLOGY, 8^{TH} ED., Lange Publishing, Los Altos, Calif. (1994)).

[00105] CTL epitope (class I epitope) (*i.e.*, $CD8^+$ T cell epitope) encoding nucleic acids preferably provide an epitope peptide of about eight to about thirteen amino acids in length (*e.g.*, 8, 9, 10, 11, 12 or 13), more preferably about eight to about eleven amino acids in length, and most preferably about nine amino acids in length. HTL ($CD4^+$ T-cell) epitope nucleic acids can provide an epitope peptide of about seven to about twenty three (*e.g.*, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22 or 23) preferably about seven to about seventeen (*e.g.*, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17, more preferably about eleven to about fifteen (*e.g.*, 11, 12, 13, 14 or 15), and most preferably about thirteen amino acids in length.

[00106] "Degenerate binding" indicates that a peptide is bound by more than one HLA molecule; a synonym is "cross reactive binding." "Cross reactive binding" may also be used to define the interaction of an antigen with multiple populations of antibodies. In certain preferred embodiments, epitopes disclosed herein do not exhibit cross reactive or degenerate binding. Other embodiments encompass degenerate or cross reactive binding of antigens or epitopes.

[00107] With regard to a particular amino acid sequence, an "epitope" is a set of amino acid residues that is involved in recognition by a particular immunoglobulin, or in the context of T cells, those residues necessary for recognition by T cell receptor proteins and/or Major Histocompatibility Complex (MHC) receptors. In an immune system setting, *in vitro* or *in vivo*, an epitope is the collective features of a molecule, such as primary, secondary and tertiary peptide structure, and charge, that together form a site recognized by an immunoglobulin, T cell receptor or HLA molecule. Throughout this

disclosure epitope and peptide are often used interchangeably. It is to be appreciated, however, that isolated or purified protein or peptide molecules larger than and comprising an epitope of the invention are still within the bounds of the invention.

[00108] A "flanking" or "linking" residue is a residue that is positioned next to an epitope. A flanking residue can be introduced or inserted at a position adjacent to the N-terminus or the C-terminus of an epitope. Flanking residues suitable for use in the subject invention are disclosed, for example, in U.S. Patent Nos. 6,419,931, which is hereby incorporated by reference in its entirety, including all sequences, figures, references, and tables.

[00109] An "immunogenic peptide" or "peptide epitope" is a peptide that comprises an allele-specific motif or supermotif such that the peptide will bind an HLA molecule and induce a CTL (or $CD8^+$ T cell) and/or HTL (or $CD4^+$ T cell) response. An "immunogenic peptide" or "peptide epitope" can also be a peptide that comprises a motif that binds to antibody molecules or B-cells found in the immune system of an individual. Thus, immunogenic peptides of the invention are capable of binding to an antibody molecule, a B-cell, or appropriate HLA molecule and thereafter inducing an immune response (*e.g.*, the induction of antibody production, a cytotoxic T cell response, or a helper T cell response) to the antigen from which the immunogenic peptide is derived.

[00110] The term "residue" refers to an amino acid or amino acid mimetic incorporated into a peptide or protein by an amide bond or amide bond mimetic.

[00111] A "spacer" or "linker" refers to a sequence that is inserted between two epitopes in a multi-epitope construct to prevent the occurrence of junctional epitopes and/or to increase the efficiency of processing. A multi-epitope construct may have one or more spacer nucleic acids. A spacer nucleic acid may flank each epitope nucleic acid in a construct, or the spacer nucleic acid to epitope nucleic acid ratio may be about 2 to 10, about 5 to 10, about 6 to 10, about 7 to 10, about 8 to 10, or about 9 to 10, where a ratio of about 8 to 10 has been determined to yield favorable results for some constructs. The spacer nucleic acid may encode one or more amino acids. A spacer nucleic acid flanking a class I HLA epitope in a multi-epitope construct is preferably between one and about eight amino acids in length. A spacer nucleic acid flanking a class II HLA epitope in a multi-epitope construct is preferably greater than five, six, seven, or more amino acids in

length, and more preferably five or six amino acids in length. The number of spacers in a construct, the number of amino acids in a spacer, and the amino acid composition of a spacer can be selected to optimize epitope processing and/or minimize junctional epitopes. It is preferred that spacers are selected by concomitantly optimizing epitope processing and junctional motifs. Suitable amino acids for optimizing epitope processing are described herein. Also, suitable amino acid spacing for minimizing the number of junctional epitopes in a construct are described herein for class I and class II HLAs. For example, spacers flanking class II HLA epitopes preferably include G, P, and/or N residues as these are not generally known to be primary anchor residues (see, *e.g.*, PCT/US00/19774). A particularly preferred spacer for flanking a class II HLA epitope includes alternating G and P residues, for example, $(GP)_n$, $(PG)_n$, $(GP)_nG$, or $(PG)_nP$, and so forth, where n is an integer between one and ten, preferably two or about two, and where a specific example of such a spacer is GPGPG.

[00112] In some multi-epitope constructs, it is sufficient that each spacer nucleic acid encodes the same amino acid sequence. In multi-epitope constructs having two spacer nucleic acids encoding the same amino acid sequence, the spacer nucleic acids encoding those spacers may have the same or different nucleotide sequences, where different nucleotide sequences may be preferred to decrease the likelihood of unintended recombination events when the multi-epitope construct is inserted into cells.

[00113] In other multi-epitope constructs, one or more of the spacer nucleic acids may encode different amino acid sequences. While many of the spacer nucleic acids may encode the same amino acid sequence in a multi-epitope construct, one, two, three, four, five or more spacer nucleic acids may encode different amino acid sequences, and it is possible that all of the spacer nucleic acids in a multi-epitope construct encode different amino acid sequences. Spacer nucleic acids may be optimized with respect to the epitope nucleic acids they flank by determining whether a spacer sequence will maximize epitope processing and/or minimize junctional epitopes, as described herein.

[00114] Multi-epitope constructs may be distinguished from one another according to whether the spacers in one construct optimize epitope processing or minimize junctional epitopes over another construct, and preferably, constructs may be distinguished where one construct is concomitantly optimized for epitope processing and junctional epitopes over the other. Computer assisted methods and *in vitro* and *in vivo*

laboratory methods for determining whether a construct is optimized for epitope processing and junctional motifs are described herein.

[00115] "Multi-epitope constructs of the invention may also be "optimized". The term "optimized" or "optimizing" refers to increasing the immunogenicity or antigenicity of a multi-epitope construct having at least one epitope pair by sorting epitopes to minimize the occurrence of junctional epitopes, inserting flanking residues that flank the C-terminus or N-terminus of an epitope, and inserting spacer residue to further prevent the occurrence of junctional epitopes or to provide a flanking residue. An increase in immunogenicity or antigenicity of an optimized multi-epitope construct is measured relative to a multi-epitope construct that has not been constructed based on the optimization parameters and is using assays known to those of skill in the art, *e.g.*, assessment of immunogenicity in HLA transgenic mice, ELISPOT, interferon-gamma release assays, tetramer staining, chromium release assays, and presentation on dendritic cells.

[00116] The subject invention also concerns antibodies that bind to polypeptides of the invention. Antibodies that are immunospecific for the malarial polypeptides set forth herein are specifically contemplated. In various embodiments, antibodies which do not cross react with other proteins or malarial proteins are also specifically contemplated. The antibodies of the subject invention can be prepared using standard materials and methods known in the art (see, for example, *Monoclonal Antibodies: Principles and Practice*, 1983; *Monoclonal Hybridoma Antibodies: Techniques and Applications*, 1982; *Selected Methods in Cellular Immunology*, 1980; *Immunological Methods, Vol. II*, 1981; *Practical Immunology*, and Kohler *et al.* [1975] *Nature* 256:495).

[00117] The term "antibody" is used in the broadest sense and specifically covers monoclonal antibodies (including full length monoclonal antibodies), polyclonal antibodies, multispecific antibodies (*e.g.*, bispecific antibodies), and antibody fragments so long as they exhibit the desired biological activity, particularly neutralizing activity. "Antibody fragments" comprise a portion of a full length antibody, generally the antigen binding or variable region thereof. Examples of antibody fragments include Fab, Fab', $F(ab')_2$, and Fv fragments; diabodies; linear antibodies; single-chain antibody molecules; and multi-specific antibodies formed from antibody fragments.

[00118] The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to conventional (polyclonal) antibody preparations that typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. The modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by the hybridoma method first described by Kohler *et al.* [1975] *Nature* 256: 495, or may be made by recombinant DNA methods (see, *e.g.*, U.S. Pat. No. 4,816,567). The "monoclonal antibodies" may also be isolated from phage antibody libraries using the techniques described in Clackson *et al.* [1991] *Nature* 352: 624-628 and Marks *et al.* [1991] *J. Mol. Biol.* 222: 581-597, for example.

[00119] The monoclonal antibodies described herein specifically include "chimeric" antibodies (immunoglobulins) in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (U.S. Pat. No. 4,816,567; and Morrison *et al.* [1984] *Proc. Natl. Acad Sci. USA* 81: 6851-6855). Also included are humanized antibodies, such as those taught in U.S. Patent Nos. 6,407,213 or 6,417,337 which are hereby incorporated by reference in their entirety.

[00120] "Single-chain Fv" or "sFv" antibody fragments comprise the V_H and V_L domains of an antibody, wherein these domains are present in a single polypeptide chain. Generally, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For

a review of sFv see Pluckthun in The Pharmacology of Monoclonal Antibodies [1994] Vol. 113:269-315, Rosenburg and Moore eds. Springer-Verlag, New York.

[00121] The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy chain variable domain (V_H) connected to a light chain variable domain (V_L) in the same polypeptide chain (V_H -V_L). Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger *et al.* [1993] *Proc. Natl. Acad. Sci. USA* 90: 6444-6448. The term "linear antibodies" refers to the antibodies described in Zapata *et al.* [1995] *Protein Eng.* 8(10):1057-1062.

[00122] An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody *in situ* within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

[00123] The terms "comprising", "consisting of" and "consisting essentially of" are defined according to their standard meaning. The terms may be substituted for one another throughout the instant application in order to attach the specific meaning associated with each term. The phrases "isolated" or "biologically pure" refer to material that is substantially or essentially free from components which normally accompany the material as it is found in its native state. Thus, isolated peptides in accordance with the invention preferably do not contain materials normally associated with the peptides in their *in situ* environment. "Link" or "join" refers to any method known in the art for functionally connecting peptides, including, without limitation, recombinant fusion,

covalent bonding, disulfide bonding, ionic bonding, hydrogen bonding, and electrostatic bonding.

[00124] Following are examples which illustrate procedures for practicing the invention. These examples should not be construed as limiting. All percentages are by weight and all solvent mixture proportions are by volume unless otherwise noted.

[00125] In this disclosure, "binding data" results are often expressed in terms of "IC_{50}'s." IC_{50} is the concentration of peptide in a binding assay at which 50% inhibition of binding of a reference peptide is observed. Given the conditions in which the assays are run (*i.e.*, limiting HLA proteins and labeled peptide concentrations), these values approximate KD values. Assays for determining binding are described in detail, *e.g.*, in PCT publications WO 94/20127 and WO 94/03205 (each of which is hereby incorporated by reference in its entirety). It should be noted that IC_{50} values can change, often dramatically, if the assay conditions are varied, and depending on the particular reagents used (*e.g.*, HLA preparation, etc.). For example, excessive concentrations of HLA molecules will increase the apparent measured IC_{50} of a given ligand. Alternatively, binding is expressed relative to a reference peptide. Although as a particular assay becomes more, or less, sensitive, the IC_{50}'s of the peptides tested may change somewhat, the binding relative to the reference peptide will not significantly change. For example, in an assay run under conditions such that the IC_{50} of the reference peptide increases 10-fold, the IC_{50} values of the test peptides will also shift approximately 10-fold. Therefore, to avoid ambiguities, the assessment of whether a peptide is a good, intermediate, weak, or negative binder is generally based on its IC_{50}, relative to the IC_{50} of a standard peptide. Binding may also be determined using other assay systems including those using: live cells (*e.g.*, Ceppellini *et al.*, Nature 339:392, 1989; Christnick *et al.*, Nature 352:67, 1991; Busch *et al.*, Int. Immunol. 2:443, 19990;Hill *et al.*, J. Immunol. 147:189,1991;del Guercio *et al.*, J. Immunol. 154:685, 1995), cell free systems using detergent lysates (*e.g.*, Cerundolo *et al.*, J. Immunol. 21:2069, 1991), immobilized purified MHC (*e.g.*, Hill *et al.*, J. Immunol. 152, 2890, 1994; Marshall *et al.*, J. Immunol. 152:4946, 1994), ELISA systems (*e.g.*, Reay *et al.*, EMBO J. 11:2829, 1992), surface plasmon resonance (*e.g.*, Khilko *et al.*, J. Biol. Chem. 268:15425, 1993); high flux soluble phase assays (Hammer *et al.*, J. Exp. Med. 180:2353, 1994), and measurement of class I MHC stabilization or assembly (*e.g.*, Ljunggren *et al.*, Nature 346:476, 1990; Schumacher *et al.*, Cell 62:563,

1990; Townsend *et al.*, Cell 62:285, 1990; Parker *et al.*, J. Immunol. 149:1896, 1992). Predicted IC_{50} values may be referred to as PIC values and measured IC_{50} values may be referred to a MIC values.

Example 1

[00126] Starting with 27 open reading frames defined by Multidimensional Protein Identification Technology, 9 highly antigenic proteins were identified. These highly antigenic proteins were recognized by volunteers immunized with irradiated sporozoites; mock immunized individuals (controls) failed to recognize these proteins. Several of these nine proteins were more antigenic than previously well-characterized proteins.

[00127] To identify and prioritize a set of ORFs representing antigens potentially expressed in the sporozoite and intrahepatic stage of the parasite life cycle, MS/MS spectra of peptide sequences generated by Multidimensional Protein Identification Technology (MudPIT) (Washburn, M.P., Wolters, D., & Yates, J.R. 3rd. Large-scale analysis of the yeast proteome by multidimensional protein identification technology. *Nat. Biotechnol.* 19, 242-247 (2001)) of *P. falciparum* sporozoite preparations were scanned against the *P. falciparum* genomic sequence database using SEQUEST™ software (Florens, L. *et al.* A proteomic view of the *Plasmodium falciparum* life cycle. *Submitted*). A panel of 27 ORF's (10 expressed only in sporozoites, and 17 common to other stages of the parasite life cycle) were selected. Their size ranged between 96 - 4544 amino acids (mean 1252), the percentage of the protein covered by identified peptides ranged between 0.5 - 49.5%, and the frequency of recognition in the *P. falciparum* proteome dataset ranged between 16 peptide hits from 6 different sporozoite runs (antigen 2) to single peptide hits (antigens 1, 11, 14, 16, 19 and 25. When searched against the final *P. falciparum* database using refined gene model predictions, and taking into consideration genomic sequence information from the *Anopheles* (vector) and human (host) databases, 19 of the 27 antigens could be identified using stringent selection criteria and six others could be identified only with relaxed criteria.

[00128] Amino acid sequences from the 27 ORFs were scanned with HLA-A1, A2, A3/A11, A24 and DR supertype PIC algorithms; a total of 3241 peptides were identified (range = 14-435; mean = 120 sequences per antigen). A set of 1142 sequences was synthesized (range = 13-50; mean = 42), selecting the top 10 scorers per supertype

per antigen for larger ORFs. Control sets of peptides were synthesized from 4 known antigens (PfCSP, PfSSP2, PfLSA1 and PfEXP1). Next, predicted epitopes were tested for their capacity to induce recall IFN-γ immune responses using PBMC from volunteers immunized with irradiated *P. falciparum* sporozoites and either protected (n=4) or not protected (n=4) against challenge with infectious sporozoites, or control volunteers mock immunized in parallel (n=4) (see Table 1). Peptides were tested as pools, at 1 μg/ml each peptide with each antigen represented by a separate pool, by IFN-γ ELIspot (Washburn, M.P., Wolters, D., &Yates, J.R. 3rd. Large-scale analysis of the yeast proteome by multidimensional protein identification technology. *Nat. Biotechnol.* **19**, 242-247 (2001)). Positive and negative control epitopes from well characterized antigens (CMV, Influenza, EBV, HIV) were also included.

[00129] Considering a stimulation index (ratio test response/control) > 2.0 as positive, 19 of the 27 unknown antigens were recognized by at least 1 of 8 irradiated sporozoite immunized volunteers, but not by any of the 4 mock immunized controls (Table 1). Nine of the 27 antigens (#2, 5, 3, 18, 22, 21, 13, 11, 20) were recognized by at least 50% of irradiated sporozoite volunteers in at least 25% of assays, 3 antigens (#1, 12, 17) were recognized by at least 25% of volunteers in at least 15% of assays, and 7 antigens (#6, 7, 9, 14, 15, 16, 19) were recognized by at least 10% volunteers in at least 5% of assays. Eight of the 27 unknown antigens (#4, 8, 10, 23, 24, 25, 26, 27) failed to induce IFN-γ responses of sufficient magnitude to meet our criteria of positivity. Pools of predicted epitopes from the known antigens, PfCSP, PfSSP2, PfLSA1 and PfEXP1, were also recognized by irradiated sporozoite volunteers although the frequency of response to those pools was somewhat lower than that to pools of peptides representing previously validated epitopes derived from the same antigens (Doolan, D.L. *et al.* Degenerate cytotoxic T cell epitopes from P. falciparum restricted by multiple HLA-A and HLA-B supertype alleles. Immunity. 7, 97-112 (1997); Doolan, D.L. *et al.* HLA-DR-promiscuous T cell epitopes from *Plasmodium* flaciparum pre-erthrocytic-stage antigens restricted by multiple HLA class II alleles. J Immunol. 165:1123-1137 (2000); Wang, R., *et al.* Induction of CD4(+) T cell-dependent CD8(+) type 1 responses in humans by a malaria DNA vaccine. *Proc. Natl. Acad. Sci. U.S.*A. **98**, 10817-10822 (2001)) (Table 1). Particularly noteworthy, the reactivity against several of the newly identified antigens greatly exceeded the reactivities observed against all 4 known antigens For example, both

antigens 2 and 5 were recognized by 7/8 irradiated sporozoite volunteers in 9/16 assays, and antigens 3 and 18 were recognized by 6/8 irradiated sporozoite volunteers in 6/16 assays.

[00130] Results show that HLA-A2 peptide pools from antigens 2, 5 and 13, and HLA-A1 and HLA-DR peptide pools from antigens 2 and 5, are recognized by irradiated sporozoite volunteers who express the respective HLA alleles, but not by mock immunized controls. Deconvolution at the level of individual epitopes is in progress. Additionally, a comprehensive analysis of HLA binding against the A1, A2, A3/11, A24, and DR1 supertypes has been completed for selected antigens. Several degenerate binders have been identified for each supertype/antigen combination, and 50 to 70% of the predicted peptides have been identified as degenerate HLA binders.Further analysis also revealed that the antigenicity results correlate to a large degree with the proteomic data. For example, of 9 antigens associated with high immune reactivity, 7 were identified by multiple peptide hits in multiple MudPIT runs

[00131] All patents, patent applications, provisional applications, polynucleotide sequences, amino acid sequences, tables and publications referred to or cited herein are incorporated by reference in their entirety, including all figures, to the extent they are not inconsistent with the explicit teachings of this specification. It should be understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application.

Table 1. Summary of immune reactivities against the panel of 27 putative antigens and 4 known antigens.

Antigen	IRRADIATED SPOROZOITE IMMUNIZED						MOCK IMMUNIZED	
	# vol respond	% vol respond	# assays	% assays	SI respond	SFC respond	# vol respond	# assays
1	3	37.5	3	18.75	2.5	59.3	0	0
2	8	100	9	56.25	2.9	110.4	0	0
3	6	75	6	37.5	2.6	119.1	0	0
4	0	-	-	-	-	-	0	0
5	7	87.5	9	56.25	2.8	101.8	0	0
6	1	12.5	1	6.25	2.4	88.3	0	0
7	1	12.5	1	6.25	2.1	43.3	0	0
8	0	-	-	-	-	-	0	0
9	2	25	2	12.5	2.5	32.0	0	0
10	0	-	-	-	-	-	0	0
11	4	50	4	25	3.1	81.3	0	0
12	3	37.5	3	18.75	2.2	48.2	0	0
13	4	50	5	31.25	2.9	92.2	0	0
14	1	12.5	1	6.25	2.2	55.3	0	0
15	2	25	2	12.5	2.5	28.8	0	0
16	2	25	2	12.5	2.2	27.2	0	0
17	3	37.5	3	18.75	2.4	57.6	0	0
18	6	75	6	37.5	2.2	58.4	0	0
19	2	25	2	12.5	2.7	31.3	0	0
20	4	50	4	25	2.5	74.8	0	0
21	4	50	5	31.25	2.3	48.2	0	0
22	5	62.5	5	31.25	2.9	108.4	0	0
23	0	-	-	-	-	-	0	0
24	0	-	-	-	-	-	0	0
25	0	-	-	-	-	-	0	0
26	0	-	-	-	-	-	0	0
27	0	-	-	-	-	-	0	0
TOTAL UNKNOWNS	1-8	44.7	3.8	24.0	2.5	66.6		
"HIGH"	4-8	66.7	5.9	36.8	2.7	88.3		
"INTERMEDIATE"	3	37.5	3.0	18.8	2.4	55.0		
"LOW"	1-2	19.6	1.6	9.8	2.4	43.8		
Range	1-8	12.5-100	1-9	6.25-56.25	2.1-3.1	27.2-110.4		
KNOWNS (@1ug/ml) predicted	1.4	17.2	1.4	8.6	2.9	57.3		
Range	1-3	12.5-37.5	1-3	6.25-18.75	2.0-3.4	30.5-137.4		
KNOWNS (@1ug/ml) validated	4.0	50.0	3.8	23.4	3.5	64.0		
Range	3-5	37.5-62.5	3-6	18.75-37.5	3.5-3.6	46.6-91.4		
TOTAL KNOWNS (@1ug/ml)	2.3	28.1	2.2	13.5	3.2	60.0		
Range	1-5	12.5-62.5	1-6	6.25-37.5	2.0-3.6	30.5-137.4		
TOTAL KNOWNS (@10ug/ml)	4-8	81.3	7.8	60.9	11.1	588.2		
CMV/EBV/Flu	7	87.5	12.0	50.0	4.0	59.0	4	100

Table 2:
Pf-derived A1 supertype peptides with PIC <20nM

Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	PIC A*0101 PIC	A*0201	A*1101	PIC A*2402 PIC
331.t00003	Chromosome10		216	98.0038	KTNKWEDIY	9	15.962	1000000.0	1475.7	1000000.0
331.t00003	Chromosome10		790	98.0039	KSIYIFYTY	9	10.624	1000000.0	34.6	1000000.0
331.t00003	Chromosome10		986	98.0040	GTFTFQNMY	9	6.439	1000000.0	51.0	1000000.0
331.t00003	Chromosome10		1298	98.0041	CNDGNILYY	9	5.246	1000000.0	1000000.0	1000000.0
331.t00003	Chromosome10		1379	98.0042	YFECIMKLY	9	8.786	1000000.0	39035.2	242.6
331.t00003	Chromosome10		1389	98.0043	VYEGKLKKY	9	18.802	1000000.0	1000000.0	1753.1
331.t00003	Chromosome10		1650	98.0001	VVDLFCGVGY	10	9.498	1000000.0	153.7	1000000.0
331.t00003	Chromosome10		1770	98.0044	FSSINTYDY	9	4.161	1000000.0	4680.1	1000000.0
331.t00003	Chromosome10		1803	98.0045	VSNVEDSNY	9	18.299	1000000.0	11308.4	1000000.0
331.t00003	Chromosome10		1831	98.0046	NSNYNKKLY	9	19.200	1000000.0	4533.0	1000000.0
18.000811	Chr12Contig18		182	98.0047	KVSDEIWNY	9	6.117	1000000.0	40.5	1000000.0
MY924Fe3.p1t1			92	98.0048	ISGEGLIIY	9	4.901	1000000.0	2464.4	1000000.0
MY924Fe3.p1t1			215	98.0002	FVEDSSSFLY	10	8.740	1000000.0	445.2	1000000.0
MY924Fe3.p1t1			384	98.0049	DSDSSNVLY	9	7.960	1000000.0	22156.1	1000000.0
MY924Fe3.p1t1			561	98.0050	SQDVFIIEY	9	6.978	1000000.0	117.2	1000000.0
MY924Fe3.p1t1			1028	98.0051	NSMFHIIMY	9	4.429	1000000.0	243.3	1000000.0
MY924Fe3.p1t1			1093	98.0052	SSYNLFEEY	9	6.022	1000000.0	82.2	1000000.0
MY924Fe3.p1t1			1258	98.0053	SSGKTFICY	9	2.145	1000000.0	264.3	1000000.0
MY924Fe3.p1t1			1340	98.0054	ILENILLSY	9	3.307	1000000.0	8368.7	1000000.0
MY924Fe3.p1t1			1439	98.0055	FSDLILYVY	9	2.218	1000000.0	4308.8	1000000.0
MY924Fe3.p1t1			2318	98.0056	HIENILLKY	9	2.560	1000000.0	10911.0	1000000.0
MP03001	MAL3P2.11	CAB38998	14	98.0057	FVEALFQEY	9	1.370	1000000.0	698.4	1000000.0
MP03001	MAL3P2.11	CAB38998	310	98.0058	PSDKHIKEY	9	18.149	1000000.0	150075.4	1000000.0
1369.t00001	Chromosome 11		38	98.0059	IMNHLMTLY	9	9.966	1000000.0	224.2	1019.1
1369.t00001	Chromosome 11		149	98.0060	LIENELMNY	9	18.117	1000000.0	15763.1	1000000.0
1369.t00001	Chromosome 11		182	98.0061	NVDQQNDMY	9	6.934	1000000.0	6419.6	1000000.0
1369.t00001	Chromosome 11		309	98.0062	SSFFMNRFY	9	17.546	1000000.0	48.4	1000000.0
1369.t00001	Chromosome 11		342	98.0063	NHEQKLSEY	9	16.912	1000000.0	1000000.0	1000000.0

Table 2:
Pf-derived A1 supertype peptides with PIC <20nM

Docket No.: EPI-103X

Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	PIC A*0101 PIC	A*0201	A*1101	A*2402 PIC
1369.t00001	Chromosome 11		347	98.0003	LSEYYDXDIY	10	18.838	1000000.0	3608.2	1000000.0
1369.t00001	Chromosome 11		363	98.0064	QEEQKKYIY	9	19.642	1000000.0	1000000.0	1000000.0
699.t00001	Chromosome 11		313	98.0065	DSQNELTNY	9	19.647	1000000.0	97274.6	1000000.0
699.t00001	Chromosome 11		441	98.0004	FSFFFSLIDY	10	1.491	1000000.0	319.3	1000000.0
699.t00001	Chromosome 11		480	98.0066	CHEMKAEFY	9	15.998	1000000.0	1000000.0	1000000.0
699.t00001	Chromosome 11		548	98.0067	MFSSIFENY	9	6.908	1000000.0	1357.8	2826.7
699.t00001	Chromosome 11		749	98.0068	NSLILLNLY	9	11.791	1000000.0	4626.8	1000000.0
699.t00001	Chromosome 11		859	98.0069	YIDNDINIY	9	12.867	1000000.0	52350.4	1000000.0
699.t00001	Chromosome 11		919	98.0070	EEDKTYELY	9	13.159	1000000.0	1000000.0	1000000.0
699.t00001	Chromosome 11		922	98.0071	KTYELYQKY	9	7.495	1000000.0	22.4	1000000.0
699.t00001	Chromosome 11		1013	98.0072	CTHISYYKY	9	14.092	1000000.0	406.1	1000000.0
699.t00001	Chromosome 11		1046	98.0005	FVDEEGEQLY	10	6.559	1000000.0	5771.7	1000000.0
M13Hg2.q1t3			8	98.0073	NSLYNKIEY	9	19.553	1000000.0	3889.9	1000000.0
M13Hg2.q1t3			46	98.0006	YSSASESNFY	10	12.365	1000000.0	5058.0	1000000.0
M13Hg2.q1t3			49	98.0074	ASESNFYKY	9	1.848	1000000.0	630.5	1000000.0
M13Hg2.q1t3			196	98.0075	ASGKLFSLY	9	2.466	1000000.0	266.9	1000000.0
M13Hg2.q1t3			237	98.0076	GSNKVSDWY	9	16.782	1000000.0	1646.1	1000000.0
M13Hg2.q1t3			511	98.0007	FQDNYLKLDY	10	7.493	1000000.0	19742.1	1000000.0
M13Hg2.q1t3			597	98.0008	FFDYNSQYYY	10	19.854	1000000.0	2749.2	1043.1
M13Hg2.q1t3			597	98.0077	FFDYNSQYY	9	11.735	1000000.0	3766.2	160.3
M13Hg2.q1t3			699	98.0078	MLEQKLSNY	9	1.204	1000000.0	13925.8	1000000.0
M13Hg2.q1t3			882	98.0079	NSFNNSNIY	9	16.821	1000000.0	5231.6	1000000.0
Mal_5L10c4.q1t6			8	98.0080	CSSTKDLNY	9	2.097	1000000.0	16168.9	1000000.0
Mal_5L10c4.q1t6			263	98.0081	YDDDKYNKY	9	7.997	1000000.0	98918.2	1000000.0
Mal_5L10c4.q1t6			638	98.0082	GTYGNMENY	9	2.825	1000000.0	209.0	1000000.0
Mal_5L10c4.q1t6			690	98.0083	FTYYSCKNY	9	6.979	1000000.0	257.7	1000000.0
Mal_5L10c4.q1t6			1022	98.0084	YDERNTLVY	9	5.181	1000000.0	47876.1	1000000.0
Mal_5L10c4.q1t6			1387	98.0085	STDDSKNVY	9	4.783	1000000.0	2220.4	1000000.0

Table 2:
Pf-derived A1 supertype peptides with PIC <20nM

Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	PIC A*0101 PIC	A*0201	A*1101	A*2402 PIC
Mal_5L10c4.q1t6			1451	98.0086	FSDDNKNLY	9	2.622	1000000.0	56737.7	1000000.0
Mal_5L10c4.q1t6			1508	98.0009	YLDNELTINY	10	6.162	1000000.0	7177.6	1000000.0
Mal_5L10c4.q1t6			1709	98.0087	STTSLNYHY	9	7.670	1000000.0	19.1	1000000.0
Mal_5L10c4.q1t6			1907	98.0088	GLDLKMTLY	9	2.747	1000000.0	5170.0	1000000.0
571.t00003	Chromosome11		1044	98.0010	YTFQNNNDFY	10	2.179	1000000.0	93.5	1000000.0
571.t00003	Chromosome11		1080	98.0089	HTNNKTSIY	9	4.189	1000000.0	1677.3	1000000.0
571.t00003	Chromosome11		1710	98.0090	FVDPNKYIY	9	2.171	1000000.0	6898.3	1000000.0
571.t00003	Chromosome11		1827	98.0011	NVEAYHNDNY	10	5.835	1000000.0	1804.6	1000000.0
571.t00003	Chromosome11		1858	98.0091	YSNNSHAEY	9	7.282	1000000.0	662.3	1000000.0
571.t00003	Chromosome11		1905	98.0092	LTNNSSYIY	9	7.415	1000000.0	186.2	1000000.0
571.t00003	Chromosome11		2211	98.0093	SSSIYNQNY	9	6.330	1000000.0	318.5	1000000.0
571.t00003	Chromosome11		2476	98.0094	GSYGTFLKY	9	1.127	1000000.0	151.7	1000000.0
571.t00003	Chromosome11		2532	98.0095	DIDKTVLHY	9	4.678	1000000.0	10960.5	1000000.0
571.t00003	Chromosome11		2571	98.0012	FNDTQKKGTY	10	7.668	1000000.0	1000000.0	1000000.0
MP03072	PFC0450w	CAA15614	95	98.0013	LSASDEYEQY	10	14.664	1000000.0	11938.7	1000000.0
MP03072	PFC0450w	CAA15614	96	98.0096	SASDEYEQY	9	16.603	1000000.0	163.8	1000000.0
45.t00001	Chromosome14		13	98.0014	FQAAESNERY	10	13.667	1000000.0	5804.6	1000000.0
45.t00001	Chromosome14		14	98.0097	QAAESNERY	9	7.537	1000000.0	4581.2	1000000.0
45.t00001	Chromosome14		81	98.0015	ELEASISGKY	10	17.550	1000000.0	30954.5	1000000.0
45.t00001	Chromosome14		82	98.0098	LEASISGKY	9	18.208	1000000.0	1000000.0	1000000.0
45.t00001	Chromosome14		188	98.0099	NLALLYGEY	9	12.836	1000000.0	4104.6	1000000.0
MP03137	PFC0700c	CAB11150	14	98.0100	SSPLFNNFY	9	20.002	1000000.0	464.0	1000000.0
MP03137	PFC0700c	CAB11150	69	98.0101	LNEQLIYTY	9	10.436	1000000.0	1000000.0	1000000.0
MP03137	PFC0700c	CAB11150	145	98.0102	QNADKNFLY	9	10.234	1000000.0	1000000.0	1000000.0
MP03137	PFC0700c	CAB11150	255	98.0016	FVSSIFISFY	10	10.460	1000000.0	44.6	1000000.0
MP03137	PFC0700c	CAB11150	256	98.0103	VSSIFISFY	9	15.732	1000000.0	544.5	1000000.0
12.t00018	Chromosome14		112	98.0104	YSYYEPLRY	9	4.229	1000000.0	560.9	1000000.0
12.t00018	Chromosome14		250	98.0017	KSNNIIPLLY	10	8.533	1000000.0	967.3	1000000.0

Table 2:
Pf-derived A1 supertype peptides with PIC <20nM

Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	PIC A*0101 PIC	A*0201	A*1101	A*2402 PIC
12.t00018	Chromosome14		467	98.0105	SSSDEENLY	9	8.006	1000000.0	2243.6	1000000.0
12.t00018	Chromosome14		468	98.0106	SSDEENLYY	9	6.105	1000000.0	64.6	1000000.0
12.t00018	Chromosome14		607	98.0107	KSNMNNNLY	9	6.927	1000000.0	923.1	1000000.0
12.t00018	Chromosome14		626	98.0108	FYDKRFIFY	9	4.639	1000000.0	1000000.0	18.3
12.t00018	Chromosome14		696	98.0018	NVEKNFLLYY	10	7.724	1000000.0	328.7	1000000.0
12.t00018	Chromosome14		696	98.0109	NVEKNFLLY	9	0.789	1000000.0	1330.7	1000000.0
12.t00018	Chromosome14		949	98.0110	KMDSFLNVY	9	6.016	1000000.0	1384.3	151.9
12.t00018	Chromosome14		1042	98.0111	NSLIEFLFY	9	9.105	1000000.0	774.9	1000000.0
mal_BU121g9.q1c1			80	98.0112	ATYKNGNIY	9	3.423	1000000.0	290.6	1000000.0
mal_9A57b11.q1t2			226	98.0113	DEEKIFVKY	9	18.436	1000000.0	1000000.0	1000000.0
mal_BL50e8.p1ca_5			86	98.0114	HTSNDSGSY	9	7.801	1000000.0	10632.6	1000000.0
mal_BL50e8.p1ca_5			136	98.0019	FSFTVGEGKY	10	4.464	1000000.0	4191.1	1000000.0
mal_BL50e8.p1ca_5			186	98.0115	ETNNNLFIY	9	3.940	1000000.0	574.3	1000000.0
mal_BL50e8.p1ca_5			319	98.0116	HVSKHAFEY	9	3.473	1000000.0	286.4	1000000.0
mal_BL50e8.p1ca_5			387	98.0117	MSGYSSNNY	9	4.983	1000000.0	1178.7	1000000.0
mal_BL50e8.p1ca_5			460	98.0118	FMESAFVNY	9	2.609	1000000.0	3568.1	1208.1
mal_BL50e8.p1ca_5			650	98.0119	RSPCSHKLY	9	6.243	1000000.0	805.6	1000000.0
mal_BL50e8.p1ca_5			679	98.0020	FTGENNIERY	10	15.909	1000000.0	1908.1	1000000.0
mal_BL50e8.p1ca_5			777	98.0120	NTLMLKADY	9	15.648	1000000.0	6774.7	1000000.0
mal_BL50e8.p1ca_5			880	98.0121	VSSKPANEY	9	15.176	1000000.0	3405.9	1000000.0
M13S8h6.p1t_3			57	98.0122	ITYSFTVSY	9	10.960	1000000.0	25.1	1000000.0
M13S8h6.p1t_3			233	98.0123	LVETLDNLY	9	3.907	1000000.0	24044.7	1000000.0
M13S8h6.p1t_3			235	98.0124	ETLDNLYLY	9	2.901	1000000.0	801.6	1000000.0
M13S8h6.p1t_3			295	98.0125	LSAKYYISY	9	4.669	1000000.0	635.7	1000000.0
M13S8h6.p1t_3			551	98.0126	HSDIHLLNY	9	1.423	1000000.0	5008.9	1000000.0
M13S8h6.p1t_3			676	98.0021	FTSPVNIKEY	10	10.972	1000000.0	1911.2	1000000.0
M13S8h6.p1t_3			746	98.0127	YSSYSSPKY	9	5.286	1000000.0	6184.9	1000000.0
M13S8h6.p1t_3			898	98.0128	GMERNKTKY	9	7.244	1000000.0	88038.7	24764.5

Table 2:
Pf-derived A1 supertype peptides with PIC <20nM

Docket No.: EPI-103X

Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	PIC A*0101 PIC	A*0201	A*1101	A*2402 PIC
M13S8h6.plt_3			1268	98.0129	YSNIDSGKY	9	11.517	1000000.0	14325.6	1000000.0
M13S8h6.plt_3			1488	98.0130	LIDLSCIHY	9	3.960	1000000.0	1722.8	1000000.0
585.t00002	Chromosome11		297	98.0131	CSDSSLNIY	9	2.643	1000000.0	44436.7	1000000.0
585.t00002	Chromosome11		381	98.0132	VSFDNNENY	9	7.080	1000000.0	824.4	1000000.0
585.t00002	Chromosome11		465	98.0022	YTDIIINIRY	10	1.851	1000000.0	1716.6	1000000.0
585.t00002	Chromosome11		575	98.0023	LSNIRKPLFY	10	5.132	1000000.0	3669.8	1000000.0
585.t00002	Chromosome11		741	98.0133	NVDANYCKY	9	3.822	1000000.0	813.1	1000000.0
585.t00002	Chromosome11		1021	98.0134	CVEKNNMSY	9	6.497	1000000.0	33246.6	1000000.0
585.t00002	Chromosome11		1161	98.0135	SSDGKKSEY	9	5.530	1000000.0	8369.5	1000000.0
585.t00002	Chromosome11		1219	98.0136	RSNNFFFSY	9	6.117	1000000.0	11.9	1000000.0
585.t00002	Chromosome11		1361	98.0024	FTMVYEKIKY	10	2.669	1000000.0	726.8	1000000.0
585.t00002	Chromosome11		1739	98.0137	NVDIFLHYY	9	3.691	1000000.0	42.6	1000000.0
1223.t00015	mal_9A21f9.qlt_4		387	98.0138	SSNEIHNFY	9	7.488	1000000.0	19.5	1000000.0
1223.t00015	mal_9A21f9.qlt_4		1065	98.0139	GTKLNRTKY	9	6.438	1000000.0	9805.4	1000000.0
1223.t00015	mal_9A21f9.qlt_4		1583	98.0025	ATVSRAGIVY	10	9.716	1000000.0	351.9	1000000.0
1223.t00015	mal_9A21f9.qlt_4		1833	98.0140	YTLSSGTKY	9	4.847	1000000.0	1878.1	1000000.0
1223.t00015	mal_9A21f9.qlt_4		2309	98.0141	VSEKEQQLY	9	6.585	1000000.0	56024.7	1000000.0
1223.t00015	mal_9A21f9.qlt_4		2426	98.0142	VVDFERLRY	9	3.185	1000000.0	457.2	1000000.0
1223.t00015	mal_9A21f9.qlt_4		2778	98.0143	FIDLYKQMY	9	5.792	1000000.0	14889.5	1000000.0
1223.t00015	mal_9A21f9.qlt_4		3445	98.0144	IVDITNVNY	9	6.389	1000000.0	1065.1	1000000.0
1223.t00015	mal_9A21f9.qlt_4		4163	98.0145	LEDVKKILY	9	9.183	1000000.0	1000000.0	1000000.0
1223.t00015	mal_9A21f9.qlt_4		4267	98.0146	SLDIPDIAY	9	9.566	1000000.0	1095.4	1000000.0
599.t00001	Chromosome11		26	98.0147	SSCQNSLNY	9	1.030	1000000.0	86.7	1000000.0
599.t00001	Chromosome11		183	98.0148	KSDITNLNY	9	4.923	1000000.0	947.1	1000000.0
599.t00001	Chromosome11		304	98.0149	ETNNGDLKY	9	6.392	1000000.0	6561.2	1000000.0
599.t00001	Chromosome11		430	98.0150	LSEDNKNRY	9	7.171	1000000.0	178412.8	1000000.0
599.t00001	Chromosome11		1018	98.0026	LLDLRKNGLY	10	3.696	1000000.0	12286.3	1000000.0
599.t00001	Chromosome11		1412	98.0027	GVDKSLKIMY	10	8.185	1000000.0	3010.4	1000000.0

Table 2:
Pf-derived A1 supertype peptides with PIC <20nM

Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	PIC A*0101 PIC	A*0201	A*1101	A*2402 PIC
599.t00001	Chromosome11		1427	98.0151	YTPTNKEMY	9	6.553	1000000.0	73406.9	1000000.0
599.t00001	Chromosome11		1516	98.0028	ESANDSTNYY	10	6.672	1000000.0	2007.1	1000000.0
599.t00001	Chromosome11		1662	98.0152	LSNSITVSY	9	9.278	1000000.0	771.6	1000000.0
599.t00001	Chromosome11		1902	98.0153	GTTQSNNIY	9	3.444	1000000.0	4003.2	1000000.0
MP01072	M1045c5.p1c.C_6		27	98.0154	SDDEIIIIY	9	11.359	1000000.0	1265.6	1000000.0
MP01072	M1045c5.p1c.C_6		41	98.0155	ISSNGKLNY	9	6.926	1000000.0	2877.4	1000000.0
MP01072	M1045c5.p1c.C_6		60	98.0156	GSIQNAYLY	9	2.697	1000000.0	389.5	1000000.0
MP01072	M1045c5.p1c.C_6		381	98.0157	GTMRNRKKY	9	1.998	1000000.0	249.1	1000000.0
MP01072	M1045c5.p1c.C_6		707	98.0158	KSLLKNYNY	9	15.958	1000000.0	419.1	1000000.0
MP01072	M1045c5.p1c.C_6		725	98.0159	NVEDTNMLY	9	9.314	1000000.0	3255.4	1000000.0
MP01072	M1045c5.p1c.C_6		1065	98.0029	NTDNKDVLNY	10	6.923	1000000.0	6127.0	1000000.0
MP01072	M1045c5.p1c.C_6		1253	98.0160	HTITISQKY	9	3.528	1000000.0	4947.2	1000000.0
MP01072	M1045c5.p1c.C_6		1257	98.0161	ISQKYTSSY	9	13.157	1000000.0	5019.1	1000000.0
MP01072	M1045c5.p1c.C_6		1336	98.0030	KTFHRILAVY	10	13.836	1000000.0	85.1	1000000.0
PIR2	T28161		228	98.0162	KTNGAEERY	9	8.691	1000000.0	326.3	1000000.0
PIR2	T28161		293	98.0163	GTVPTNLDY	9	3.979	1000000.0	793.4	1000000.0
PIR2	T28161		403	98.0031	ESSQNSPKNY	10	8.536	1000000.0	24883.8	1000000.0
PIR2	T28161		639	98.0032	QTDFQGWGHY	10	2.601	1000000.0	1349.4	1000000.0
PIR2	T28161		899	98.0164	EADFIKKMY	9	9.348	1000000.0	113941.0	1000000.0
PIR2	T28161		917	98.0165	ATICRAMKY	9	5.412	1000000.0	112.4	1000000.0
PIR2	T28161		1192	98.0033	KTDEQYNENY	10	5.386	1000000.0	1911.8	1000000.0
PIR2	T28161		1201	98.0034	YTFKNPPPQY	10	8.064	1000000.0	918.8	1000000.0
PIR2	T28161		1884	98.0166	WLEYFLDDY	9	8.602	1000000.0	35096.0	1000000.0
PIR2	T28161		2221	98.0167	ITSSSESEY	9	9.299	1000000.0	1168.0	1000000.0
55.t00004	Chromosome14		45	98.0168	YVDIGSNIY	9	3.352	1000000.0	18704.2	1000000.0
55.t00004	Chromosome14		457	98.0169	DTCKNIWNY	9	3.842	1000000.0	878.3	1000000.0
55.t00004	Chromosome14		563	98.0170	LSQGKKNTY	9	10.561	1000000.0	40514.9	1000000.0
55.t00004	Chromosome14		928	98.0171	NIDCVISPY	9	8.449	1000000.0	3464.1	1000000.0

Table 2:
Pf-derived A1 supertype peptides with PIC <20nM

Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	PIC A*0101 PIC	A*0201	A*1101	PIC A*2402 PIC
55.t00004	Chromosome14		953	98.0172	NMDNLLFTY	9	5.144	1000000.0	413.3	6464.5
55.t00004	Chromosome14		1105	98.0035	FVDHNYNYNY	10	6.601	1000000.0	687.9	1000000.0
55.t00004	Chromosome14		1261	98.0173	HSKENQQKY	9	3.798	1000000.0	41445.3	1000000.0
55.t00004	Chromosome14		1339	98.0174	VSEGYTSTY	9	7.735	1000000.0	4760.1	1000000.0
55.t00004	Chromosome14		1358	98.0175	FMDSQNGMY	9	8.455	1000000.0	21913.6	2720.6
55.t00004	Chromosome14		1537	98.0036	NSYNDSLINY	10	12.536	1000000.0	1846.9	1000000.0
13.t00011	Chromosome14		27	98.0176	STGINEENY	9	6.590	1000000.0	838.9	1000000.0
13.t00011	Chromosome14		44	98.0177	MNETVFLDY	9	5.456	1000000.0	1000000.0	1000000.0
13.t00011	Chromosome14		77	98.0178	LTSKVWDTY	9	6.496	1000000.0	616.6	1000000.0
37.t00002	Chromosome14		10	98.0179	KHDALTYMY	9	23.541	1000000.0	1000000.0	1000000.0
37.t00002	Chromosome14		14	98.0180	LTYMYCVYY	9	10.044	1000000.0	20.3	1000000.0
674.t00001	Chromosome11		201	98.0181	NIDINDLGY	9	10.069	1000000.0	23874.2	1000000.0
674.t00001	Chromosome11		260	98.0182	ISSNQFNNY	9	6.099	1000000.0	2575.9	1000000.0
674.t00001	Chromosome11		400	98.0183	DIEPLISSY	9	14.646	1000000.0	183727.1	1000000.0
674.t00001	Chromosome11		453	98.0037	VTNNDSINNY	10	17.920	1000000.0	1310.7	1000000.0
674.t00001	Chromosome11		772	98.0184	ESGKNMEHY	9	8.198	1000000.0	75390.5	1000000.0
674.t00001	Chromosome11		868	98.0185	LKDFDMLLY	9	12.047	1000000.0	1000000.0	1000000.0
674.t00001	Chromosome11		936	98.0186	YIDVEDDDY	9	13.870	1000000.0	377275.0	1000000.0
674.t00001	Chromosome11		1001	98.0187	DMDDNYYLY	9	3.056	1000000.0	2478.6	45380.9
674.t00001	Chromosome11		1224	98.0188	YGDNNKDCY	9	19.772	1000000.0	368191.0	1000000.0
674.t00001	Chromosome11		1239	98.0189	IYDFNNNSY	9	17.735	1000000.0	1000000.0	365.4

Table 3:
Pf-derived A24 supertype peptides with PIC <100nM

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	A*0101 PIC	A*0201	A*1101	A*2402 PIC
331.t00003	Chromosome10		10	98.0206	FYKKKRNVL	9	67134.0	1000000.0	1000000.0	1.708
331.t00003	Chromosome10		110	98.0207	VYEINKNEF	9	84.1	1000000.0	1000000.0	2.011
331.t00003	Chromosome10		604	98.0208	FFVWGHDMF	9	221.0	1000000.0	1000000.0	3.642
331.t00003	Chromosome10		684	98.0209	VYNIKENFW	9	123239.4	1000000.0	1000000.0	2.687
331.t00003	Chromosome10		1108	98.0210	KYNLCHNML	9	147073.6	1000000.0	1000000.0	0.324
331.t00003	Chromosome10		1268	98.0211	FYVPIKKKL	9	172677.3	1000000.0	1000000.0	2.705
331.t00003	Chromosome10		1365	98.0212	KYEIIGNIL	9	89209.4	1000000.0	1000000.0	1.961
331.t00003	Chromosome10		1449	98.0213	FWLAIKDIF	9	173.9	1000000.0	1000000.0	1.093
331.t00003	Chromosome10		1515	98.0214	LYRRRKNLF	9	113.5	1000000.0	1000000.0	1.220
331.t00003	Chromosome10		1704	98.0215	IYIIKQNSF	9	111.6	1000000.0	1000000.0	0.256
18.000811	Chr12Contig18		5	98.0190	LFVCFLIFHF	10	672.3	1000000.0	1000000.0	19.783
18.000811	Chr12Contig18		8	98.0191	CFLIFHFFLF	10	1385.7	1000000.0	1000000.0	18.444
18.000811	Chr12Contig18		8	98.0216	CFLIFHFFL	9	106491.6	1000000.0	1000000.0	0.321
18.000811	Chr12Contig18		11	98.0217	IFHFFLFLL	9	53306.2	1000000.0	1000000.0	38.527
18.000811	Chr12Contig18		13	98.0192	HFFLFLLYIL	10	1000000.0	1000000.0	1000000.0	35.659
18.000811	Chr12Contig18		13	98.0218	HFFLFLLYI	9	24845.8	1000000.0	1000000.0	26.159
18.000811	Chr12Contig18		14	98.0219	FFLFLLYIL	9	62569.1	1000000.0	1000000.0	32.471
18.000811	Chr12Contig18		19	98.0220	LYILFLVKM	9	90645.8	1000000.0	1000000.0	63.051
18.000811	Chr12Contig18		41	98.0221	VFLVFSNVL	9	178682.3	1000000.0	1000000.0	5.555
18.000811	Chr12Contig18		160	98.0222	TYGIIVPVL	9	123562.9	1000000.0	1000000.0	3.015
MY924Fe3.pltl			153	98.0223	FFNVFNIFF	9	45.6	1000000.0	1000000.0	0.470
MY924Fe3.pltl			1412	98.0224	FYSWLQNVL	9	83170.3	1000000.0	1000000.0	2.428
MY924Fe3.pltl			1435	98.0225	FYERFSDLI	9	46149.1	1000000.0	1000000.0	0.625
MY924Fe3.pltl			1534	98.0226	VYLIQNNYI	9	615175.4	1000000.0	1000000.0	0.632
MY924Fe3.pltl			1557	98.0227	NYMKNSFYI	9	24802.7	1000000.0	1000000.0	2.200
MY924Fe3.pltl			1800	98.0228	VYCNYVTEI	9	160654.7	1000000.0	1000000.0	3.071

Table 3:
Pf-derived A24 supertype peptides with PIC <100nM

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	A*0101 PIC	A*0201	A*1101	A*2402 PIC
MY924Fe3.p1t1			1839	98.0229	HYEVLPYKF	9	14.6	1000000.0	1000000.0	2.621
MY924Fe3.p1t1			1846	98.0230	KFTIIVESL	9	181796.5	1000000.0	1000000.0	1.946
MY924Fe3.p1t1			2159	98.0231	FMTRAHFHI	9	9020.6	52.2	1000000.0	1.455
MY924Fe3.p1t1			2380	98.0232	FYKSKVIII	9	53263.7	1000000.0	1000000.0	0.928
MP03001	MAL3P2.11	CAB38998	11	98.0233	SFLFVEALF	9	80.3	1000000.0	1000000.0	53.045
MP03001	MAL3P2.11	CAB38998	54	98.0234	YYGKQENWY	9	73.1	1000000.0	1000000.0	49.750
MP03001	MAL3P2.11	CAB38998	369	98.0235	KMEKCSSVF	9	34.0	1000000.0	1000000.0	39.989
MP03001	MAL3P2.11	CAB38998	376	98.0236	VFNVVNSSI	9	231723.3	1000000.0	1000000.0	82.506
1369.t00001	Chromosome 11		34	98.0237	NYMKIMNHL	9	37582.2	1000000.0	1000000.0	4.875
1369.t00001	Chromosome 11		225	98.0193	SYKSSKRDKF	10	1632.7	1000000.0	1000000.0	46.746
1369.t00001	Chromosome 11		264	98.0238	TYKKKNNHI	9	90904.7	1000000.0	1000000.0	12.042
1369.t00001	Chromosome 11		277	98.0239	VYYNILIVL	9	59837.4	1000000.0	1000000.0	11.637
1369.t00001	Chromosome 11		285	98.0240	LYYLFNQHI	9	56431.2	1000000.0	1000000.0	5.598
1369.t00001	Chromosome 11		310	98.0241	SFFMNRFYI	9	56480.3	1000000.0	1000000.0	80.940
1369.t00001	Chromosome 11		316	98.0242	FYITTRYKY	9	45.2	1000000.0	1000000.0	3.968
1369.t00001	Chromosome 11		328	98.0243	KYINFINFI	9	289163.4	1000000.0	1000000.0	0.095
1369.t00001	Chromosome 11		331	98.0244	NFINFIKVL	9	610070.5	1000000.0	1000000.0	37.188
1369.t00001	Chromosome 11		380	98.0245	KYEALIKLL	9	105887.8	1000000.0	1000000.0	9.605
699.t00001	Chromosome 11		443	98.0246	FFFSLIDYF	9	118.9	1000000.0	1000000.0	1.331
699.t00001	Chromosome 11		460	98.0247	KYNIKVCEL	9	98354.1	1000000.0	1000000.0	0.429
699.t00001	Chromosome 11		487	98.0248	FYLYISFLL	9	34312.8	1000000.0	1000000.0	0.417
699.t00001	Chromosome 11		664	98.0249	FYTNNANLL	9	42910.8	1000000.0	1000000.0	0.639
699.t00001	Chromosome 11		766	98.0250	EYNPSFFYL	9	22929.4	1000000.0	1000000.0	1.772
699.t00001	Chromosome 11		845	98.0251	SFIIFKNIF	9	249.9	1000000.0	1000000.0	3.449
699.t00001	Chromosome 11		881	98.0252	LYMNFLKFI	9	34148.2	1000000.0	1000000.0	4.363
699.t00001	Chromosome 11		929	98.0253	KYLIILLYI	9	93640.1	1000000.0	1000000.0	1.034

Table 3:
Pf-derived A24 supertype peptides with PIC <100nM

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	A*0101 PIC	A*0201	A*1101	A*2402 PIC
699.t00001	Chromosome 11		1020	98.0254	KYIYIYIYI	9	215740.5	1000000.0	1000000.0	0.296
699.t00001	Chromosome 11		1024	98.0255	IYIYIFIYL	9	52331.1	1000000.0	1000000.0	2.300
M13Hg2.q1t3			135	98.0256	IYINKLSFF	9	67.4	1000000.0	1000000.0	3.329
M13Hg2.q1t3			142	98.0257	FFSIKDELF	9	27.2	1000000.0	1000000.0	14.276
M13Hg2.q1t3			156	98.0258	EFLKNNSYF	9	164.9	1000000.0	1000000.0	20.204
M13Hg2.q1t3			163	98.0259	YFNIIQQKI	9	45274.1	1000000.0	1000000.0	13.888
M13Hg2.q1t3			244	98.0260	WYCSACNFL	9	56993.5	1000000.0	1000000.0	7.339
M13Hg2.q1t3			296	98.0261	LYLINNKNL	9	150801.1	1000000.0	1000000.0	28.854
M13Hg2.q1t3			345	98.0262	TYKDANNNI	9	71978.1	1000000.0	1000000.0	29.035
M13Hg2.q1t3			521	98.0263	VYEKEKQYF	9	103.6	1000000.0	1000000.0	3.963
M13Hg2.q1t3			553	98.0194	PYFNFFVNYF	10	185.8	1000000.0	1000000.0	33.503
M13Hg2.q1t3			889	98.0264	IYNNNNEHI	9	77962.6	1000000.0	1000000.0	24.919
Mal_5L10c4.q1t6			78	98.0265	EYNKYNEYF	9	90.4	1000000.0	1000000.0	3.130
Mal_5L10c4.q1t6			137	98.0266	NYVNNNNVF	9	220.5	1000000.0	1000000.0	3.441
Mal_5L10c4.q1t6			321	98.0267	KYPIKYCEL	9	183114.8	1000000.0	1000000.0	0.364
Mal_5L10c4.q1t6			416	98.0268	AYHDLIKLF	9	66.8	1000000.0	1000000.0	4.671
Mal_5L10c4.q1t6			533	98.0269	KYISSVNYF	9	194.8	1000000.0	1000000.0	0.018
Mal_5L10c4.q1t6			773	98.0270	KYDWFFNSF	9	34.0	1000000.0	1000000.0	0.374
Mal_5L10c4.q1t6			1183	98.0271	HYVIKKYII	9	133499.1	1000000.0	1000000.0	1.507
Mal_5L10c4.q1t6			1259	98.0272	LYLHIHKLF	9	72.0	1000000.0	1000000.0	0.343
Mal_5L10c4.q1t6			1323	98.0273	YYRTNYGYI	9	165642.6	1000000.0	1000000.0	4.072
Mal_5L10c4.q1t6			2054	98.0274	KYLRYHSQL	9	421667.1	1000000.0	1000000.0	0.655
571.t00003	Chromosome11		74	98.0275	FYIDKCIHF	9	23.2	1000000.0	1000000.0	0.120
571.t00003	Chromosome11		162	98.0276	FYTNYYQSF	9	48.3	1000000.0	1000000.0	0.186
571.t00003	Chromosome11		177	98.0277	PYINQTNIF	9	228.9	1000000.0	1000000.0	0.527
571.t00003	Chromosome11		807	98.0278	NYPNNANHI	9	176667.0	1000000.0	1000000.0	3.103

Table 3:
Pf-derived A24 supertype peptides with PIC <100nM

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	A*0101 PIC	A*0201	A*1101	A*2402 PIC
571.t00003	Chromosome11		834	98.0279	TYNNFHNSY	9	52.4	1000000.0	1000000.0	0.776
571.t00003	Chromosome11		1917	98.0280	YMNNNTYSF	9	7.7	1000000.0	1000000.0	2.132
571.t00003	Chromosome11		2026	98.0281	KYTEGATNF	9	74.8	1000000.0	1000000.0	1.964
571.t00003	Chromosome11		2450	98.0282	FYISIIDII	9	150563.0	1000000.0	1000000.0	1.632
571.t00003	Chromosome11		2540	98.0283	YYKEHISEF	9	96.3	1000000.0	1000000.0	3.143
571.t00003	Chromosome11		2914	98.0284	YYNRANNEI	9	46291.4	1000000.0	1000000.0	3.342
MP03072	PFC0450w	CAA15614	17	98.0285	AFLLITFLM	9	37258.4	1000000.0	1000000.0	17.525
MP03072	PFC0450w	CAA15614	53	98.0195	LYVIFLVLLF	10	174.0	1000000.0	1000000.0	16.581
MP03072	PFC0450w	CAA15614	53	98.0286	LYVIFLVLL	9	107336.6	1000000.0	1000000.0	5.089
MP03072	PFC0450w	CAA15614	86	98.0287	KYVQLASTY	9	65.1	1000000.0	1000000.0	70.547
45.t00001	Chromosome14		21	98.0196	RYQDPQNYEL	10	1000000.0	1000000.0	1000000.0	46.471
45.t00001	Chromosome14		40	98.0288	IYYFDGNSW	9	97026.0	1000000.0	1000000.0	15.493
45.t00001	Chromosome14		94	98.0289	VYRHCEYIL	9	560574.8	1000000.0	1000000.0	27.538
45.t00001	Chromosome14		135	98.0290	TWKPTIFLL	9	34068.5	1000000.0	1000000.0	26.741
45.t00001	Chromosome14		168	98.0291	SYKVNCINF	9	25.3	1000000.0	1000000.0	63.592
45.t00001	Chromosome14		216	98.0292	KYNYFIHFF	9	39.1	1000000.0	1000000.0	0.380
45.t00001	Chromosome14		218	98.0293	NYFIHFFTW	9	95820.5	1000000.0	1000000.0	2.156
45.t00001	Chromosome14		222	98.0294	HFFTWGTMF	9	17.4	1000000.0	1000000.0	6.418
45.t00001	Chromosome14		229	98.0295	MFVPKYFEL	9	57423.3	1000000.0	1000000.0	28.589
45.t00001	Chromosome14		295	98.0296	IYTIIQDQL	9	334935.0	1000000.0	1000000.0	9.774
MP03137	PFC0700c	CAB11150	3	98.0197	DFFLKSKFNI	10	1000000.0	1000000.0	1000000.0	79.527
MP03137	PFC0700c	CAB11150	4	98.0297	FFLKSKFNI	9	80470.7	1000000.0	1000000.0	10.043
MP03137	PFC0700c	CAB11150	9	98.0298	KFNILSSPL	9	275819.0	1000000.0	1000000.0	48.661
MP03137	PFC0700c	CAB11150	61	98.0299	RMTSLKNEL	9	45471.5	1089.6	1000000.0	50.292
MP03137	PFC0700c	CAB11150	77	98.0300	YYNNFNNNY	9	29.9	1000000.0	1000000.0	2.802
MP03137	PFC0700c	CAB11150	87	98.0301	YYNKSTEKL	9	25069.1	1000000.0	1000000.0	6.131

Table 3:
Pf-derived A24 supertype peptides with PIC <100nM

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	A*0101 PIC	A*0201	A*1101	A*2402 PIC
MP03137	PFC0700c	CAB11150	109	98.0302	EYEPTANLL	9	29899.8	1000000.0	1000000.0	9.359
12.t00018	Chromosome14		479	98.0303	PYEEVENYF	9	118.2	1000000.0	1000000.0	3.525
12.t00018	Chromosome14		506	98.0304	KFILHMTLL	9	418744.3	1000000.0	1000000.0	7.942
12.t00018	Chromosome14		544	98.0305	NFLNIYASL	9	309896.9	1000000.0	1000000.0	7.653
12.t00018	Chromosome14		594	98.0306	VWKKLIEYF	9	120.2	1000000.0	1000000.0	7.058
12.t00018	Chromosome14		614	98.0307	LYVSMYIPF	9	113.5	1000000.0	1000000.0	6.679
12.t00018	Chromosome14		618	98.0308	MYIPFIKKF	9	62.3	1000000.0	1000000.0	2.663
12.t00018	Chromosome14		625	98.0309	KFYDKRFIF	9	53.3	1000000.0	1000000.0	1.395
12.t00018	Chromosome14		675	98.0310	IYNMYHNNF	9	27.2	1000000.0	1000000.0	0.737
12.t00018	Chromosome14		678	98.0311	MYHNNFSYF	9	61.8	1000000.0	1000000.0	5.105
12.t00018	Chromosome14		815	98.0312	KYDITKNLI	9	86746.4	1000000.0	1000000.0	2.983
mal_BU121g9.q1c1			61	98.0313	GYFKRIFKL	9	39278.5	1000000.0	1000000.0	64.889
mal_BU121g9.q1c1			81	98.0314	TYKNGNIYI	9	240142.1	1000000.0	1000000.0	20.110
mal_BU121g9.q1c1			87	98.0315	IYIYIYIYI	9	133656.3	1000000.0	1000000.0	2.246
mal_BU121g9.q1c1			89	98.0198	IYIYIYIYFL	10	1000000.0	1000000.0	1000000.0	72.026
mal_BU121g9.q1c1			89	98.0316	IYIYIYIYF	9	89.8	1000000.0	1000000.0	0.543
mal_9A57b11.q1t2			75	98.0317	IFKNDNNTF	9	290.7	1000000.0	1000000.0	11.568
mal_9A57b11.q1t2			103	98.0318	KYGNICHHI	9	61693.1	1000000.0	1000000.0	4.552
mal_9A57b11.q1t2			139	98.0319	QYTDIPSLI	9	41835.9	1000000.0	1000000.0	24.727
mal_9A57b11.q1t2			159	98.0320	VFCYEYFIF	9	98.9	1000000.0	1000000.0	69.226
mal_9A57b11.q1t2			161	98.0199	CYEYFIFDIF	10	811.1	1000000.0	1000000.0	61.974
mal_9A57b11.q1t2			161	98.0321	CYEYFIFDI	9	32300.1	1000000.0	1000000.0	79.659
mal_9A57b11.q1t2			171	98.0322	KYARNILSL	9	27927.9	1000000.0	1000000.0	3.398
mal_9A57b11.q1t2			230	98.0323	IFVKYLPLF	9	68.2	1000000.0	1000000.0	30.518
mal_9A57b11.q1t2			233	98.0324	KYLPLFLMM	9	16925.5	1000000.0	1000000.0	15.776
mal_9A57b11.q1t2			237	98.0325	LFLMMEHSF	9	51.0	1000000.0	1000000.0	70.804

Table 3:
Pf-derived A24 supertype peptides with PIC <100nM

							PIC			
Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	A*0101 PIC	A*0201	A*1101	A*2402 PIC
mal_BL50e8.plca_5			116	98.0326	QYSNYFDYL	9	103941.7	1000000.0	1000000.0	17.499
mal_BL50e8.plca_5			184	98.0327	PYETNNNLF	9	37.2	1000000.0	1000000.0	4.367
mal_BL50e8.plca_5			341	98.0328	YYSRRVEKI	9	33168.4	1000000.0	1000000.0	6.349
mal_BL50e8.plca_5			555	98.0329	KFKWIQDNL	9	453346.6	1000000.0	1000000.0	30.007
mal_BL50e8.plca_5			687	98.0200	RYVGLGSFHF	10	1143.3	1000000.0	1000000.0	33.267
mal_BL50e8.plca_5			768	98.0330	TYKMYPPEF	9	68.2	1000000.0	1000000.0	7.746
mal_BL50e8.plca_5			771	98.0331	MYPPEFNTL	9	37286.8	1000000.0	1000000.0	14.291
mal_BL50e8.plca_5			827	98.0332	KYCIGSTYF	9	184.3	1000000.0	1000000.0	0.261
mal_BL50e8.plca_5			833	98.0333	TYFLRQVSI	9	163553.3	1000000.0	1000000.0	31.623
mal_BL50e8.plca_5			857	98.0334	KYSARLHPI	9	52609.1	1000000.0	1000000.0	33.171
M13S8h6.plt_3			152	98.0335	FYLKKKFLF	9	30.5	1000000.0	1000000.0	0.091
M13S8h6.plt_3			298	98.0336	KYYISYKVL	9	328554.4	1000000.0	1000000.0	3.468
M13S8h6.plt_3			321	98.0337	KYINKNISL	9	213679.4	1000000.0	1000000.0	0.395
M13S8h6.plt_3			380	98.0338	KYLKEDNTF	9	189.5	1000000.0	1000000.0	2.580
M13S8h6.plt_3			753	98.0339	KYGDNENNF	9	50.4	1000000.0	1000000.0	2.048
M13S8h6.plt_3			1208	98.0340	VFTKINNLF	9	55.7	1000000.0	1000000.0	4.101
M13S8h6.plt_3			1438	98.0341	IWLIRSIYL	9	175087.7	1000000.0	1000000.0	2.659
M13S8h6.plt_3			1444	98.0342	IYLFIITYI	9	153399.4	1000000.0	1000000.0	4.385
M13S8h6.plt_3			1536	98.0343	FFFVFFYIF	9	26.2	1000000.0	1000000.0	0.631
M13S8h6.plt_3			1541	98.0344	FYIFLIYSF	9	60.5	1000000.0	1000000.0	0.315
585.t00002	Chromosome11		1	98.0345	MYIFFFILF	9	12.6	1000000.0	1000000.0	1.911
585.t00002	Chromosome11		11	98.0346	FYVMSTYTF	9	45.7	1000000.0	1000000.0	0.144
585.t00002	Chromosome11		512	98.0347	RYCTKCFLW	9	31357.1	1000000.0	1000000.0	1.726
585.t00002	Chromosome11		605	98.0348	VYAKNIPLW	9	36459.4	1000000.0	1000000.0	1.882
585.t00002	Chromosome11		663	98.0349	FFCIFFISL	9	35177.1	1000000.0	1000000.0	1.436
585.t00002	Chromosome11		681	98.0350	PYYKKKNLF	9	53.3	1000000.0	1000000.0	2.732

Table 3:
Pf-derived A24 supertype peptides with PIC <100nM

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	A*0101 PIC	A*0201	A*1101	A*2402 PIC
585.t00002	Chromosome11		1378	98.0351	FYTLVNILI	9	40959.2	1000000.0	1000000.0	2.113
585.t00002	Chromosome11		1419	98.0352	YFIIRSYEL	9	135598.6	1000000.0	1000000.0	2.721
585.t00002	Chromosome11		1483	98.0353	KYICLTCAF	9	30.1	1000000.0	1000000.0	0.435
585.t00002	Chromosome11		1752	98.0354	KYDLFNNFI	9	83062.5	1000000.0	1000000.0	1.355
1223.t00015	mal_9A21f9.q1t_4		1202	98.0355	KYKDMAKIF	9	215.2	1000000.0	1000000.0	0.315
1223.t00015	mal_9A21f9.q1t_4		1599	98.0356	GYRPFIYSW	9	83421.5	1000000.0	1000000.0	3.292
1223.t00015	mal_9A21f9.q1t_4		1621	98.0357	LYAIFNKLF	9	57.9	1000000.0	1000000.0	0.212
1223.t00015	mal_9A21f9.q1t_4		1631	98.0358	FYLDKIQIL	9	36632.3	1000000.0	1000000.0	0.942
1223.t00015	mal_9A21f9.q1t_4		2272	98.0359	RMEDKTFSL	9	8870.6	143.4	1000000.0	4.349
1223.t00015	mal_9A21f9.q1t_4		2702	98.0360	IYNCVTINW	9	10684.6	1000000.0	1000000.0	2.727
1223.t00015	mal_9A21f9.q1t_4		3109	98.0361	RWTDDSNNF	9	60.4	1000000.0	1000000.0	1.600
1223.t00015	mal_9A21f9.q1t_4		3735	98.0362	FFYDILNVI	9	40209.1	1000000.0	1000000.0	5.095
1223.t00015	mal_9A21f9.q1t_4		3968	98.0363	KYRKIIYSL	9	215862.1	1000000.0	1000000.0	0.665
1223.t00015	mal_9A21f9.q1t_4		4515	98.0364	KYFIFRIHL	9	114989.5	1000000.0	1000000.0	0.325
599.t00001	Chromosome11		8	98.0365	KYLTINFFI	9	160943.0	1000000.0	1000000.0	0.123
599.t00001	Chromosome11		14	98.0366	FFILLTLVF	9	30.5	1000000.0	1000000.0	3.495
599.t00001	Chromosome11		24	98.0367	KYSSCQNSL	9	213208.8	1000000.0	1000000.0	0.906
599.t00001	Chromosome11		955	98.0368	KFIEHINEF	9	278.8	1000000.0	1000000.0	1.175
599.t00001	Chromosome11		1118	98.0369	KYIELNDLI	9	231736.4	1000000.0	1000000.0	1.464
599.t00001	Chromosome11		1194	98.0370	PYSNVTYVI	9	97127.6	1000000.0	1000000.0	1.861
599.t00001	Chromosome11		1434	98.0371	MYDILNAYF	9	42.0	1000000.0	1000000.0	1.204
599.t00001	Chromosome11		1769	98.0372	HYIMNNTIF	9	38.3	1000000.0	1000000.0	1.389
599.t00001	Chromosome11		1929	98.0373	FFKYIISYF	9	126.1	1000000.0	1000000.0	3.000
599.t00001	Chromosome11		1943	98.0374	KYLNDDNYL	9	679247.8	1000000.0	1000000.0	0.368
MP01072	M1045c5.p1c.C_6		67	98.0375	LYKSIFKAF	9	52.5	1000000.0	1000000.0	21.749
MP01072	M1045c5.p1c.C_6		107	98.0376	SYRIVNAGF	9	268.7	1000000.0	1000000.0	7.480

Table 3:
Pf-derived A24 supertype peptides with PIC <100nM

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	A*0101 PIC	A*0201	A*1101	A*2402 PIC
MP01072	M1045c5.p1c.C_6		319	98.0377	KYTFRSLSI	9	63496.4	1000000.0	1000000.0	7.958
MP01072	M1045c5.p1c.C_6		388	98.0378	KYKNDSNRI	9	401700.0	1000000.0	1000000.0	6.170
MP01072	M1045c5.p1c.C_6		612	98.0379	SYIYNKNIF	9	105.6	1000000.0	1000000.0	13.043
MP01072	M1045c5.p1c.C_6		1042	98.0380	FMKNNTTLF	9	11.7	1000000.0	1000000.0	2.141
MP01072	M1045c5.p1c.C_6		1123	98.0381	HYVMINNNL	9	52910.4	1000000.0	1000000.0	3.607
MP01072	M1045c5.p1c.C_6		1163	98.0382	FFLFFSIFI	9	69264.3	1000000.0	1000000.0	2.646
MP01072	M1045c5.p1c.C_6		1249	98.0383	RYFLHTITI	9	101443.4	1000000.0	1000000.0	2.834
MP01072	M1045c5.p1c.C_6		1260	98.0384	KYTSSYDSL	9	230897.9	1000000.0	1000000.0	1.533
PIR2	T28161		243	98.0385	YYKLREDWW	9	283854.6	1000000.0	1000000.0	8.617
PIR2	T28161		304	98.0386	QYLRWFEEW	9	35188.7	1000000.0	1000000.0	14.859
PIR2	T28161		628	98.0387	HWTQIKKHF	9	30.8	1000000.0	1000000.0	11.497
PIR2	T28161		647	98.0388	HYFVLETVL	9	65432.8	1000000.0	1000000.0	12.976
PIR2	T28161		833	98.0389	RWMDTAGFI	9	32693.4	1000000.0	1000000.0	6.822
PIR2	T28161		848	98.0201	IYMPPRRQHF	10	391.2	1000000.0	1000000.0	14.666
PIR2	T28161		1024	98.0390	RWMTEWAEW	9	39609.0	1000000.0	1000000.0	3.877
PIR2	T28161		1574	98.0391	KYQYDKVKL	9	515925.0	1000000.0	1000000.0	6.877
PIR2	T28161		1681	98.0392	KYCRFYKRW	9	239673.9	1000000.0	1000000.0	3.433
PIR2	T28161		1887	98.0393	YFLDDYNKI	9	114991.6	1000000.0	1000000.0	7.588
55.t00004	Chromosome14		223	98.0394	KYELRKTSI	9	226076.9	1000000.0	1000000.0	3.213
55.t00004	Chromosome14		339	98.0395	MYKNKVDPL	9	208222.7	1000000.0	1000000.0	31.490
55.t00004	Chromosome14		455	98.0396	YYDTCKNIW	9	80910.8	1000000.0	1000000.0	11.820
55.t00004	Chromosome14		686	98.0397	KYINNMSFI	9	317672.0	1000000.0	1000000.0	1.757
55.t00004	Chromosome14		896	98.0398	LYPWKENKF	9	99.5	1000000.0	1000000.0	6.128
55.t00004	Chromosome14		973	98.0399	KWNVFNNSI	9	191824.8	1000000.0	1000000.0	0.536
55.t00004	Chromosome14		1027	98.0400	KFKIINSYI	9	648818.6	1000000.0	1000000.0	2.246
55.t00004	Chromosome14		1123	98.0401	NYAYDNIEL	9	113781.7	1000000.0	1000000.0	8.937

Table 3:
Pf-derived A24 supertype peptides with PIC <100nM

							PIC			
Malaria locus	Addn Source info	Accession No.	Position	Peptide No.	Sequence	AA	A*0101 PIC	A*0201	A*1101	A*2402 PIC
55.t00004	Chromosome14		1155	98.0402	IYTSTNNII	9	105468.3	1000000.0	1000000.0	7.723
55.t00004	Chromosome14		1268	98.0403	KYTYNINNL	9	65476.9	1000000.0	1000000.0	7.681
13.t00011	Chromosome14		68	98.0202	RYNVINHIYL	10	1000000.0	1000000.0	1000000.0	74.419
13.t00011	Chromosome14		68	98.0404	RYNVINHIY	9	26.0	1000000.0	1000000.0	55.779
13.t00011	Chromosome14		84	98.0405	TYNYLTPTL	9	75416.9	1000000.0	1000000.0	7.874
13.t00011	Chromosome14		96	98.0203	RFRVFKDYSF	10	3387.1	1000000.0	1000000.0	29.344
13.t00011	Chromosome14		99	98.0406	VFKDYSFFI	9	99598.3	1000000.0	1000000.0	7.373
13.t00011	Chromosome14		105	98.0407	FFIDEVKKI	9	230004.2	1000000.0	1000000.0	12.686
37.t00002	Chromosome14		20	98.0408	VYYDNYESL	9	72350.5	1000000.0	1000000.0	10.652
674.t00001	Chromosome11		68	98.0409	RFVEKIYYL	9	228887.0	1000000.0	1000000.0	8.045
674.t00001	Chromosome11		114	98.0410	IYINVQKNL	9	306183.0	1000000.0	1000000.0	14.033
674.t00001	Chromosome11		140	98.0411	KFYYYFKEF	9	92.8	1000000.0	1000000.0	14.487
674.t00001	Chromosome11		141	98.0204	FYYYFKEFLL	10	1000000.0	1000000.0	1000000.0	13.628
674.t00001	Chromosome11		141	98.0412	FYYYFKEFL	9	104311.6	1000000.0	1000000.0	1.300
674.t00001	Chromosome11		418	98.0413	TYIPDKKLL	9	209801.1	1000000.0	1000000.0	17.181
674.t00001	Chromosome11		461	98.0414	NYLYNKYYI	9	288938.1	1000000.0	1000000.0	5.750
674.t00001	Chromosome11		579	98.0415	NFKEQHLLF	9	72.4	1000000.0	1000000.0	38.780
674.t00001	Chromosome11		649	98.0416	HYINNKHNL	9	41447.1	1000000.0	1000000.0	10.887
674.t00001	Chromosome11		800	98.0417	LYREHSREL	9	274526.6	1000000.0	1000000.0	38.601
674.t00001	Chromosome11		1095	98.0418	NYINNNIYL	9	268777.1	1000000.0	1000000.0	3.259
674.t00001	Chromosome11		1117	98.0419	NYNQKENSF	9	40.2	1000000.0	1000000.0	27.868
674.t00001	Chromosome11		1396	98.0205	QYKVKIKPVF	10	5076.8	1000000.0	1000000.0	42.788

Table 4:
Pf-derived A2 supertype peptides with PIC <100nM

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101	A*2402
331.t00003	Chromosome10	105		99.0042	LIYPCVYEI	9	38050.5	43.8	1000000.0	1000000.0
331.t00003	Chromosome10	598		99.0043	NMNVQNFFV	9	50979.5	35.3	1000000.0	1000000.0
331.t00003	Chromosome10	605		99.0044	FVWGHDMFM	9	25516.6	18.5	1000000.0	1000000.0
331.t00003	Chromosome10	660		99.0045	QLDDKFAFI	9	3138.5	43.0	1000000.0	1000000.0
331.t00003	Chromosome10	950		99.0046	CLINHNFFM	9	63467.3	65.7	1000000.0	1000000.0
331.t00003	Chromosome10	957		99.0047	FMLVGGINI	9	11445.4	72.5	1000000.0	399.0
331.t00003	Chromosome10	1007		99.0048	YIIGGGCTV	9	19833.9	77.9	1000000.0	1000000.0
331.t00003	Chromosome10	1016		99.0049	FTFGSFFDV	9	2705.2	14.1	1000000.0	1000000.0
331.t00003	Chromosome10	1847		99.0050	NLSFAQYTL	9	22775.6	52.7	1000000.0	1000000.0
331.t00003	Chromosome10	1889		99.0051	RMYHYVVDI	9	47589.4	49.4	1000000.0	890.2
18.000811	Chr12Contig18	2		99.0001	VLRLFVCFLI	10	1000000.0	72.4	1000000.0	1000000.0
18.000811	Chr12Contig18	9		99.0002	FLIFHFFLFL	10	1000000.0	10.9	1000000.0	1000000.0
18.000811	Chr12Contig18	10		99.0003	LIFHFFLFLL	10	1000000.0	29.1	1000000.0	1000000.0
18.000811	Chr12Contig18	15		99.0004	FLFLLYILFL	10	404264.4	19.6	1000000.0	1000000.0
18.000811	Chr12Contig18	32		99.0005	RLPVICSFLV	10	1000000.0	99.3	1000000.0	1000000.0
18.000811	Chr12Contig18	35		99.0006	VICSFLVFLV	10	1000000.0	71.5	1000000.0	1000000.0
18.000811	Chr12Contig18	39		99.0007	FLVFLVFSNV	10	1000000.0	45.6	1000000.0	1000000.0
18.000811	Chr12Contig18	10		99.0052	LIFHFFLFL	9	8592.7	9.8	1000000.0	1000000.0
18.000811	Chr12Contig18	17		99.0053	FLLYILFLV	9	6742.1	1.9	1000000.0	1000000.0
18.000811	Chr12Contig18	35		99.0054	VICSFLVFL	9	43080.6	76.0	1000000.0	1000000.0
18.000811	Chr12Contig18	159		99.0055	ATYGIIVPV	9	18077.0	45.4	1000000.0	1000000.0
MY924Fe3.plt1		222		99.0008	FLYAFNKYYV	10	538964.2	15.2	1000000.0	1000000.0
MY924Fe3.plt1		127		99.0056	NMISVVYYI	9	97099.2	14.5	1000000.0	8.2
MY924Fe3.plt1		299		99.0057	SLCFYFLLL	9	2719.7	20.9	1000000.0	1000000.0
MY924Fe3.plt1		470		99.0058	ILFLHNYLL	9	31359.3	26.7	1000000.0	1000000.0
MY924Fe3.plt1		512		99.0059	YLDVYNFLL	9	4353.0	7.2	1000000.0	1000000.0
MY924Fe3.plt1		1209		99.0060	FQLYYMYYL	9	91212.8	4.0	1000000.0	1000000.0
MY924Fe3.plt1		1267		99.0061	YVMDKVLRL	9	984.8	45.3	1000000.0	1000000.0

Table 4:
Pf-derived A2 supertype peptides with PIC <100nM

							PIC		
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101	A*2402
MY924Fe3.p1t1		2260		99.0062	LLFILSHFI	9	11073.4	23.7	1000000.0	1000000.0
MY924Fe3.p1t1		2326		99.0063	YLVNYCLVV	9	16842.3	10.9	1000000.0	1000000.0
MY924Fe3.p1t1		2395		99.0064	KIYVCIYYL	9	157982.7	39.3	1000000.0	1000000.0
MP03001	MAL3P2.11	6	CAB38998	99.0009	ILSVSSFLFV	10	1000000.0	94.9	1000000.0	1000000.0
MP03001	MAL3P2.11	386	CAB38998	99.0010	LIMVLSFLFL	10	1000000.0	38.4	1000000.0	1000000.0
MP03001	MAL3P2.11	318	CAB38998	99.0065	YLNKIQNSL	9	13496.2	78.4	1000000.0	1000000.0
MP03001	MAL3P2.11	387	CAB38998	99.0066	IMVLSFLFL	9	8739.3	36.0	1000000.0	2608.6
1369.t00001	Chromosome 11	60		99.0011	VQMMIMIKFM	10	1000000.0	96.6	1000000.0	1000000.0
1369.t00001	Chromosome 11	62		99.0012	MMIMIKFMGV	10	1000000.0	47.1	1000000.0	1000000.0
1369.t00001	Chromosome 11	9		99.0067	KIYKIIIWI	9	56576.0	72.2	1000000.0	1000000.0
1369.t00001	Chromosome 11	23		99.0068	YMIKKLLKI	9	4324.7	52.7	1000000.0	788.9
1369.t00001	Chromosome 11	42		99.0069	LMTLYQIQV	9	32880.1	41.7	1000000.0	1000000.0
1369.t00001	Chromosome 11	68		99.0070	FMGVIYIMI	9	10136.0	91.9	1000000.0	58.6
1369.t00001	Chromosome 11	280		99.0071	NILIVLYYL	9	117610.0	42.8	1000000.0	1000000.0
1369.t00001	Chromosome 11	312		99.0072	FMNRFYITT	9	14073.8	47.8	1000000.0	1000000.0
699.t00001	Chromosome 11	488		99.0013	YLYISFLLLI	10	311433.0	34.2	1000000.0	1000000.0
699.t00001	Chromosome 11	1025		99.0014	YIYIFIYLFI	10	1000000.0	19.8	1000000.0	1000000.0
699.t00001	Chromosome 11	408		99.0073	LLDDYHFET	9	5923.7	39.5	1000000.0	1000000.0
699.t00001	Chromosome 11	488		99.0074	YLYISFLLL	9	2547.9	11.2	1000000.0	1000000.0
699.t00001	Chromosome 11	572		99.0075	FLTLTVYPI	9	22535.9	28.3	1000000.0	1000000.0
699.t00001	Chromosome 11	651		99.0076	FIIEILELL	9	15575.2	47.0	1000000.0	1000000.0
699.t00001	Chromosome 11	782		99.0077	LLYNHITSI	9	62668.0	50.4	1000000.0	1000000.0
699.t00001	Chromosome 11	882		99.0078	YMNFLKFIV	9	14215.9	50.3	1000000.0	1000000.0
699.t00001	Chromosome 11	1033		99.0079	FIYIWLHLI	9	6243.9	15.6	1000000.0	1000000.0
699.t00001	Chromosome 11	1039		99.0080	HLIIIFIFV	9	6908.2	11.5	1000000.0	1000000.0
M13Hg2.q1t3		576		99.0015	FLMWSSQIII	10	96042.7	91.8	1000000.0	1000000.0
M13Hg2.q1t3		96		99.0081	ILLSRFIFI	9	11278.3	22.9	1000000.0	1000000.0

Table 4:
Pf-derived A2 supertype peptides with PIC <100nM

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101	A*2402
M13Hg2.q1t3		508		99.0082	YLNFQDNYL	9	34942.8	80.6	1000000.0	1000000.0
M13Hg2.q1t3		551		99.0083	NIPYFNFFV	9	86593.7	41.8	1000000.0	1000000.0
M13Hg2.q1t3		558		99.0084	FVNYFEAVV	9	15474.4	100.0	1000000.0	1000000.0
M13Hg2.q1t3		569		99.0085	NIHCYTYFL	9	27934.2	25.6	1000000.0	1000000.0
M13Hg2.q1t3		576		99.0086	FLMWSSQII	9	5275.5	31.9	1000000.0	1000000.0
M13Hg2.q1t3		577		99.0087	LMWSSQIII	9	15320.6	46.4	1000000.0	614.0
M13Hg2.q1t3		723		99.0088	ILNKISSFV	9	17591.1	89.9	1000000.0	1000000.0
Mal_5L10c4.q1t6		334		99.0089	FVFFIIKNV	9	13366.7	53.5	1000000.0	1000000.0
Mal_5L10c4.q1t6		366		99.0090	IQICKLYHV	9	8534.4	35.2	1000000.0	1000000.0
Mal_5L10c4.q1t6		534		99.0091	YISSVNYFL	9	25585.7	24.2	1000000.0	1000000.0
Mal_5L10c4.q1t6		1205		99.0092	YLFQLVQSL	9	4424.1	26.3	1000000.0	1000000.0
Mal_5L10c4.q1t6		1240		99.0093	SIYFYWFLL	9	13813.9	27.2	1000000.0	1000000.0
Mal_5L10c4.q1t6		1260		99.0094	YLHIHKLFI	9	46175.4	47.6	1000000.0	1000000.0
Mal_5L10c4.q1t6		1596		99.0095	ILDDSINFV	9	8148.9	41.5	1000000.0	1000000.0
Mal_5L10c4.q1t6		1629		99.0096	FLPEQSYVL	9	36294.8	55.0	1000000.0	1000000.0
Mal_5L10c4.q1t6		1890		99.0097	HLVIQIIYV	9	52344.4	36.6	1000000.0	1000000.0
Mal_5L10c4.q1t6		2106		99.0098	FLSVINASV	9	15607.8	17.1	1000000.0	1000000.0
571.t00003	Chromosome11	105		99.0016	ILYPSLMPYV	10	1000000.0	81.0	1000000.0	1000000.0
571.t00003	Chromosome11	2443		99.0017	YLFGKVKFYI	10	821413.1	47.5	1000000.0	1000000.0
571.t00003	Chromosome11	68		99.0099	KLINTNFYI	9	109718.5	49.2	1000000.0	1000000.0
571.t00003	Chromosome11	92		99.0100	KTFIYSNFL	9	34260.6	95.5	1000000.0	1000000.0
571.t00003	Chromosome11	109		99.0101	SLMPYVECI	9	3307.6	80.4	1000000.0	1000000.0
571.t00003	Chromosome11	163		99.0102	YTNYYQSFI	9	14053.9	63.6	1000000.0	1000000.0
571.t00003	Chromosome11	1224		99.0103	FQWEKSNKI	9	17731.1	88.1	1000000.0	1000000.0
571.t00003	Chromosome11	1330		99.0104	FLIKLNNEI	9	32980.5	73.6	1000000.0	1000000.0
571.t00003	Chromosome11	1478		99.0105	YMYTNYLNM	9	5105.1	65.8	1000000.0	4545.4
571.t00003	Chromosome11	2286		99.0106	FQGEYVSNL	9	28240.4	61.4	1000000.0	1000000.0
MP03072	PFC0450w	7	CAA15614	99.0018	ILILIDAASV	10	1000000.0	88.5	1000000.0	1000000.0

Table 4:
Pf-derived A2 supertype peptides with PIC <100nM

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101	A*2402
MP03072	PFC0450w	19	CAA15614	99.0019	LLITFLMINL	10	1000000.0	82.3	1000000.0	1000000.0
MP03072	PFC0450w	46	CAA15614	99.0020	ALVVAIILYV	10	599232.7	38.0	1000000.0	1000000.0
MP03072	PFC0450w	50	CAA15614	99.0021	AIILYVIFLV	10	1000000.0	58.1	1000000.0	1000000.0
MP03072	PFC0450w	52	CAA15614	99.0022	ILYVIFLVLL	10	1000000.0	33.8	1000000.0	1000000.0
MP03072	PFC0450w	54	CAA15614	99.0023	YVIFLVLLFI	10	656413.8	20.3	1000000.0	1000000.0
MP03072	PFC0450w	57	CAA15614	99.0024	FLVLLFIYKA	10	139.6	80.7	498.9	1000000.0
MP03072	PFC0450w	18	CAA15614	99.0107	FLLITFLMI	9	5377.9	28.0	1000000.0	1000000.0
MP03072	PFC0450w	47	CAA15614	99.0108	LVVAIILYV	9	17753.4	20.8	1000000.0	1000000.0
MP03072	PFC0450w	50	CAA15614	99.0109	AIILYVIFL	9	35558.1	23.3	1000000.0	1000000.0
MP03072	PFC0450w	51	CAA15614	99.0110	IILYVIFLV	9	29081.2	23.4	1000000.0	1000000.0
MP03072	PFC0450w	52	CAA15614	99.0111	ILYVIFLVL	9	4626.7	49.4	1000000.0	1000000.0
MP03072	PFC0450w	55	CAA15614	99.0112	VIFLVLLFI	9	17063.1	28.6	1000000.0	1000000.0
45.t00001	Chromosome14	22		99.0113	YQDPQNYEL	9	17446.7	62.2	1000000.0	1000000.0
45.t00001	Chromosome14	134		99.0114	KTWKPTIFL	9	18939.7	82.8	1000000.0	1000000.0
45.t00001	Chromosome14	142		99.0115	LLNESNIFL	9	13381.3	66.8	1000000.0	1000000.0
45.t00001	Chromosome14	220		99.0116	FIHFFTWGT	9	54429.1	69.2	1000000.0	1000000.0
MP03137	PFC0700c	180	CAB11150	99.0117	VLFLQMMNV	9	71815.8	72.3	1000000.0	1000000.0
MP03137	PFC0700c	251	CAB11150	99.0118	NQMIFVSSI	9	39082.0	99.1	1000000.0	1000000.0
MP03137	PFC0700c	253	CAB11150	99.0119	MIFVSSIFI	9	17820.1	95.9	1000000.0	1000000.0
MP03137	PFC0700c	258	CAB11150	99.0120	SIFISFYLI	9	13357.1	72.3	1000000.0	1000000.0
MP03137	PFC0700c	293	CAB11150	99.0121	RLFEESLGI	9	22704.6	90.4	1000000.0	1000000.0
12.t00018	Chromosome14	870		99.0025	YLCLYNGLLL	10	294216.7	79.1	1000000.0	1000000.0
12.t00018	Chromosome14	1018		99.0026	YLLFFREKFL	10	1000000.0	57.8	1000000.0	1000000.0

Table 4:
Pf-derived A2 supertype peptides with PIC <100nM

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101	A*2402
12.t00018	Chromosome14	597		99.0122	KLIEYFLNM	9	8556.1	30.0	1000000.0	1000000.0
12.t00018	Chromosome14	615		99.0123	YVSMYIPFI	9	7367.7	57.9	1000000.0	1000000.0
12.t00018	Chromosome14	870		99.0124	YLCLYNGLL	9	12899.1	68.8	1000000.0	1000000.0
12.t00018	Chromosome14	893		99.0125	NIISSIFYI	9	94922.9	77.9	1000000.0	1000000.0
12.t00018	Chromosome14	907		99.0126	YLYDNYSHL	9	11094.9	55.2	1000000.0	1000000.0
12.t00018	Chromosome14	953		99.0127	FLNVYENFL	9	23398.0	34.3	1000000.0	1000000.0
12.t00018	Chromosome14	1037		99.0128	LIFGYNSLI	9	26493.2	50.1	1000000.0	1000000.0
12.t00018	Chromosome14	1047		99.0129	FLFYGCREV	9	24096.2	30.4	1000000.0	1000000.0
mal_BU121g9.q1c1		90		99.0130	YIYIYIYFL	9	32096.6	3.8	1000000.0	1000000.0
mal_BU121g9.q1c1		92		99.0131	YIYIYFLQI	9	15022.6	13.6	1000000.0	1000000.0
mal_9A57b11.q1t2		138		99.0132	KQYTDIPSL	9	184531.0	81.9	1000000.0	1000000.0
mal_9A57b11.q1t2		158		99.0133	KVFCYEYFI	9	10650.1	18.0	1000000.0	1000000.0
mal_9A57b11.q1t2		165		99.0134	FIFDIFKYA	9	21.1	20.2	44.0	1000000.0
mal_BL50e8.p1ca_5		6		99.0027	ALLSFLVVLV	10	1000000.0	42.5	1000000.0	1000000.0
mal_BL50e8.p1ca_5		65		99.0028	RQINFMETFV	10	1000000.0	54.6	1000000.0	1000000.0
mal_BL50e8.p1ca_5		4		99.0135	FVALLSFLV	9	3130.0	26.0	1000000.0	1000000.0
mal_BL50e8.p1ca_5		7		99.0136	LLSFLVVLV	9	11579.5	36.2	1000000.0	1000000.0
mal_BL50e8.p1ca_5		192		99.0137	FIYNWVLQT	9	30528.1	55.9	1000000.0	1000000.0
mal_BL50e8.p1ca_5		349		99.0138	ILIRALLSL	9	8963.2	44.4	1000000.0	1000000.0
mal_BL50e8.p1ca_5		353		99.0139	ALLSLDFSL	9	22110.4	36.6	1000000.0	1000000.0
mal_BL50e8.p1ca_5		562		99.0140	NLFGGGFYI	9	22065.3	23.4	1000000.0	1000000.0
mal_BL50e8.p1ca_5		779		99.0141	LMLKADYFI	9	22456.0	21.9	1000000.0	444.0
mal_BL50e8.p1ca_5		973		99.0142	NIYTHSVYV	9	245555.5	53.7	1000000.0	1000000.0
M13S8h6.p1t_3		7		99.0143	FVLACVLLI	9	10293.7	14.2	1000000.0	1000000.0
M13S8h6.p1t_3		23		99.0144	ATSTFFFFL	9	3703.8	20.0	1000000.0	1000000.0
M13S8h6.p1t_3		34		99.0145	FLLICGFCI	9	23058.3	21.3	1000000.0	1000000.0
M13S8h6.p1t_3		55		99.0146	VLITYSFTV	9	35516.3	7.8	1000000.0	1000000.0
M13S8h6.p1t_3		61		99.0147	FTVSYIFFM	9	18627.5	9.0	1000000.0	1000000.0

Table 4:
Pf-derived A2 supertype peptides with PIC <100nM

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101	A*2402
M13S8h6.p1t_3		77		99.0148	LLVCISILL	9	4378.4	24.2	1000000.0	1000000.0
M13S8h6.p1t_3		1447		99.0149	FIITYIWII	9	50315.1	20.9	1000000.0	1000000.0
M13S8h6.p1t_3		1469		99.0150	KMMWTIFIL	9	13621.2	14.7	1000000.0	35.6
M13S8h6.p1t_3		1538		99.0151	FVFFYIFLI	9	5681.7	3.2	1000000.0	1000000.0
M13S8h6.p1t_3		1582		99.0152	YLDRIQFLV	9	3212.4	6.0	1000000.0	1000000.0
585.t00002	Chromosome11	651		99.0029	VLSPFSLIFV	10	236320.1	33.8	1000000.0	1000000.0
585.t00002	Chromosome11	1380		99.0030	TLVNILILFL	10	1000000.0	25.5	1000000.0	1000000.0
585.t00002	Chromosome11	1406		99.0031	FVFFRFLFFV	10	132657.2	16.7	1000000.0	1000000.0
585.t00002	Chromosome11	6		99.0153	FILFYFYVM	9	18702.2	16.8	1000000.0	1000000.0
585.t00002	Chromosome11	17		99.0154	YTFCFLPVL	9	3159.4	24.6	1000000.0	1000000.0
585.t00002	Chromosome11	643		99.0155	WLFFFDLVV	9	13858.2	39.1	1000000.0	1000000.0
585.t00002	Chromosome11	661		99.0156	HLFFCIFFI	9	13336.6	6.4	1000000.0	1000000.0
585.t00002	Chromosome11	1386		99.0157	ILFLICYSI	9	18185.7	17.8	1000000.0	1000000.0
585.t00002	Chromosome11	1399		99.0158	YMFSYIPFV	9	20964.1	1.1	1000000.0	1000000.0
585.t00002	Chromosome11	1507		99.0159	YILFILFFI	9	12765.9	4.2	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	1387		99.0032	LIHDDVLLFL	10	1000000.0	32.2	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	270		99.0160	FVSFYKFEV	9	10792.4	28.2	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	811		99.0161	MLWCSMESV	9	5755.3	27.5	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	924		99.0162	KLFDAINYL	9	35603.1	20.5	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	1648		99.0163	FVMDITDSI	9	4215.8	44.1	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	1853		99.0164	MLYSIVWGL	9	18338.7	24.8	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	2301		99.0165	NIYFSYFYV	9	68948.8	41.1	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	2548		99.0166	FILEHVNSI	9	80628.8	42.2	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	3057		99.0167	SLLKAQLFV	9	12372.4	15.7	1000000.0	1000000.0
1223.t00015	mal_9A21f9.q1t_4	4419		99.0168	SLDEVVLYT	9	8137.8	46.3	1000000.0	1000000.0
599.t00001	Chromosome11	1069		99.0033	HLMHIINVFI	10	1000000.0	56.9	1000000.0	1000000.0
599.t00001	Chromosome11	1341		99.0034	FLSDYTTCSV	10	93945.4	72.2	1000000.0	1000000.0
599.t00001	Chromosome11	1458		99.0035	FLRNYVVIFI	10	615882.5	83.6	1000000.0	1000000.0

Table 4:
Pf-derived A2 supertype peptides with PIC <100nM

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101	A*2402
599.t00001	Chromosome11	9		99.0169	YLTINFFIL	9	4373.8	64.1	1000000.0	1000000.0
599.t00001	Chromosome11	883		99.0170	NMNDIENFV	9	32886.3	78.0	1000000.0	1000000.0
599.t00001	Chromosome11	1013		99.0171	FIHDILLDL	9	11903.4	46.8	1000000.0	1000000.0
599.t00001	Chromosome11	1034		99.0172	NQYAYDLKI	9	38604.8	81.2	1000000.0	1000000.0
599.t00001	Chromosome11	1718		99.0173	GLGGLLFII	9	5216.8	74.2	1000000.0	1000000.0
599.t00001	Chromosome11	1770		99.0174	YIMNNTIFT	9	4444.5	75.2	1000000.0	1000000.0
599.t00001	Chromosome11	1914		99.0175	HLFNFSNFV	9	16629.7	25.5	1000000.0	1000000.0
MP01072	M1045c5.p1c.C_6	1138		99.0036	YLIRNILMSI	10	819635.3	75.5	1000000.0	1000000.0
MP01072	M1045c5.p1c.C_6	66		99.0176	YLYKSIFKA	9	6.2	29.5	1755.3	1000000.0
MP01072	M1045c5.p1c.C_6	82		99.0177	YLDFYEFCV	9	5138.7	6.7	1000000.0	1000000.0
MP01072	M1045c5.p1c.C_6	1161		99.0178	KIFFLFFSI	9	19713.1	22.7	1000000.0	1000000.0
MP01072	M1045c5.p1c.C_6	1281		99.0179	KLNEINILL	9	15599.8	69.4	1000000.0	1000000.0
PIR2	T28161	577		99.0037	FLMFWVAHML	10	60152.9	33.4	1000000.0	1000000.0
PIR2	T28161	142		99.0180	LLAEVCYAA	9	9.8	35.1	4774.0	1000000.0
PIR2	T28161	369		99.0181	CLYVCDPYV	9	78244.5	58.0	1000000.0	1000000.0
PIR2	T28161	577		99.0182	FLMFWVAHM	9	3061.0	5.7	1000000.0	1000000.0
PIR2	T28161	642		99.0183	FQGWGHYFV	9	53546.0	13.8	1000000.0	1000000.0
PIR2	T28161	888		99.0184	FLGDVLFAA	9	6.7	8.3	2549.7	1000000.0
PIR2	T28161	892		99.0185	VLFAANYEA	9	25.8	20.9	100.0	1000000.0
PIR2	T28161	1098		99.0186	YLQAQTTAA	9	26.9	64.0	17290.2	1000000.0
PIR2	T28161	1461		99.0187	FLRQMFYTL	9	8779.8	60.8	1000000.0	1000000.0
PIR2	T28161	2149		99.0188	FAAFTYFYL	9	11639.0	45.5	1000000.0	1000000.0
55.t00004	Chromosome14	1358		99.0038	FMDSQNGMYI	10	26503.4	87.2	1000000.0	4109.6
55.t00004	Chromosome14	1542		99.0039	SLINYNKYFV	10	1000000.0	43.5	1000000.0	1000000.0
55.t00004	Chromosome14	84		99.0189	FVVAQLYEL	9	27995.5	19.7	1000000.0	1000000.0
55.t00004	Chromosome14	480		99.0190	KTFFFFSNV	9	10931.8	72.4	1000000.0	1000000.0
55.t00004	Chromosome14	1098		99.0191	IINSDDYFV	9	58940.8	86.9	1000000.0	1000000.0
55.t00004	Chromosome14	1364		99.0192	GMYILPQYV	9	18255.9	74.7	1000000.0	1000000.0

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Table 4:
Pf-derived A2 supertype peptides with PIC <100nM

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101	A*2402
674.t00001	Chromosome11	89		99.0040	ELVEFIFLLL	10	1000000.0	97.4	1000000.0	1000000.0
674.t00001	Chromosome11	281		99.0041	FLYKDVLMDI	10	358012.1	50.4	1000000.0	1000000.0
674.t00001	Chromosome11	89		99.0193	ELVEFIFLL	9	21772.0	47.1	1000000.0	1000000.0
674.t00001	Chromosome11	1102		99.0194	YLNKANPNI	9	12319.8	91.3	1000000.0	1000000.0
674.t00001	Chromosome11	1353		99.0195	FLQYRIPHM	9	33178.8	81.0	1000000.0	1000000.0
674.t00001	Chromosome11	1430		99.0196	YTVDIFCKI	9	11720.4	48.5	1000000.0	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
331.t00003	Chromosome10	354		99.0197	KFEPFIIHVK	10	1000000.0	1000000.0	26.5	1000000.0
331.t00003	Chromosome10	5		99.0294	KTMDTFYKK	9	2654.1	1000000.0	0.4	1000000.0
331.t00003	Chromosome10	208		99.0295	SFFDVSKKK	9	130857.6	1000000.0	16.4	1000000.0
331.t00003	Chromosome10	435		99.0296	LSQLVHFYK	9	29656.2	1000000.0	0.6	1000000.0
331.t00003	Chromosome10	779		99.0297	SVFVRRYIK	9	18991.0	1000000.0	0.7	1000000.0
331.t00003	Chromosome10	988		99.0298	FTFQNMYVR	9	5834.2	1000000.0	22.0	1000000.0
331.t00003	Chromosome10	1324		99.0299	SQNSNTFLK	9	10099.5	1000000.0	0.4	1000000.0
331.t00003	Chromosome10	1337		99.0300	ILFHKFLNK	9	3064.6	1000000.0	2.4	1000000.0
331.t00003	Chromosome10	1521		99.0301	NLFDENFCR	9	30418.9	1000000.0	165.9	1000000.0
331.t00003	Chromosome10	1551		99.0302	ALYEKVHGK	9	9346.6	1000000.0	4.4	1000000.0
18.000811	Chr12Contig18	17		99.0198	FLLYILFLVK	10	1000000.0	1000000.0	82.1	1000000.0
18.000811	Chr12Contig18	43		99.0199	LVFSNVLCFR	10	365585.5	1000000.0	14.5	1000000.0
18.000811	Chr12Contig18	80		99.0200	AFLESQSMNK	10	1000000.0	1000000.0	65.8	1000000.0
18.000811	Chr12Contig18	112		99.0201	TFLESSFDIK	10	1000000.0	1000000.0	323.9	1000000.0
18.000811	Chr12Contig18	116		99.0202	SSFDIKSEVK	10	1000000.0	1000000.0	34.1	1000000.0
18.000811	Chr12Contig18	18		99.0303	LLYILFLVK	9	5498.6	1000000.0	10.1	1000000.0
18.000811	Chr12Contig18	129		99.0304	KSMLKELIK	9	5942.8	1000000.0	12.7	1000000.0
18.000811	Chr12Contig18	166		99.0305	PVLTSLFNK	9	10202.9	1000000.0	10.1	1000000.0
MY924Fe3.pltl		1262		99.0203	TFICYYVMDK	10	1000000.0	1000000.0	23.0	1000000.0
MY924Fe3.pltl		155		99.0306	NVFNIFFEK	9	10371.8	1000000.0	0.2	1000000.0
MY924Fe3.pltl		220		99.0307	SSFLYAFNK	9	12434.3	1000000.0	0.1	1000000.0
MY924Fe3.pltl		1030		99.0308	MFHIIMYTK	9	208352.1	1000000.0	18.2	1000000.0
MY924Fe3.pltl		1181		99.0309	SLDDIYKYK	9	22644.9	1000000.0	2.9	1000000.0
MY924Fe3.pltl		1613		99.0310	KVVVKNLYK	9	34654.1	1000000.0	0.9	1000000.0
MY924Fe3.pltl		1853		99.0311	SLFRLGFVK	9	10283.0	1000000.0	0.2	1000000.0
MY924Fe3.pltl		2012		99.0312	SLFFNSLYY	9	4.6	1000000.0	2.6	1000000.0
MY924Fe3.pltl		2238		99.0313	ITFEKNYYR	9	21591.6	1000000.0	1.5	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
MY924Fc3.pltl		2285		99.0314	SQYEENKSK	9	139775.3	1000000.0	39.1	1000000.0
MP03001	MAL3P2.11	57	CAB38998	99.0204	KQENWYSLKK	10	1000000.0	1000000.0	50.6	1000000.0
MP03001	MAL3P2.11	335	CAB38998	99.0205	VTCGNGIQVR	10	1000000.0	1000000.0	170.6	1000000.0
MP03001	MAL3P2.11	17	CAB38998	99.0315	ALFQEYQCY	9	3.4	1000000.0	72.7	1000000.0
MP03001	MAL3P2.11	57	CAB38998	99.0316	KQENWYSLK	9	44996.2	1000000.0	173.7	1000000.0
1369.t00001	Chromosome 11	44		99.0206	TLYQIQVMKR	10	1000000.0	1000000.0	52.0	1000000.0
1369.t00001	Chromosome 11	58		99.0207	KQVQMMIMIK	10	1000000.0	1000000.0	8.7	1000000.0
1369.t00001	Chromosome 11	70		99.0208	GVIYIMIISK	10	1000000.0	1000000.0	10.6	1000000.0
1369.t00001	Chromosome 11	158		99.0209	ELFDKDTFFK	10	1000000.0	1000000.0	14.2	1000000.0
1369.t00001	Chromosome 11	18		99.0317	KTMNNYMIK	9	16730.1	1000000.0	1.1	1000000.0
1369.t00001	Chromosome 11	159		99.0318	LFDKDTFFK	9	32977.1	1000000.0	126.3	1000000.0
1369.t00001	Chromosome 11	287		99.0319	YLFNQHIKK	9	21347.4	1000000.0	8.2	1000000.0
1369.t00001	Chromosome 11	307		99.0320	MQSSFFMNR	9	12685.3	1000000.0	25.4	1000000.0
1369.t00001	Chromosome 11	315		99.0321	RFYITTRYK	9	258367.4	1000000.0	21.4	1000000.0
1369.t00001	Chromosome 11	319		99.0322	TTRYKYLNK	9	10429.2	1000000.0	4.5	1000000.0
699.t00001	Chromosome 11	464		99.0210	KVCELLGYYK	10	1000000.0	1000000.0	1.1	1000000.0
699.t00001	Chromosome 11	492		99.0211	SFLLLIVFSK	10	1000000.0	1000000.0	21.9	1000000.0
699.t00001	Chromosome 11	623		99.0212	KLLYKMNYLK	10	1000000.0	1000000.0	15.0	1000000.0
699.t00001	Chromosome 11	764		99.0213	TLEYNPSFFY	10	91.9	1000000.0	219.0	1000000.0
699.t00001	Chromosome 11	782		99.0214	LLYNHITSIK	10	1000000.0	1000000.0	12.1	1000000.0
699.t00001	Chromosome 11	878		99.0215	LFYLYMNFLK	10	1000000.0	1000000.0	8.2	1000000.0
699.t00001	Chromosome 11	386		99.0323	KQNIPIYIY	9	57.8	1000000.0	175.4	1000000.0
699.t00001	Chromosome 11	507		99.0324	KTNIFFKKK	9	23058.6	1000000.0	1.5	1000000.0
699.t00001	Chromosome 11	734		99.0325	IVNDLGIFY	9	2.4	1000000.0	16.6	1000000.0
699.t00001	Chromosome 11	769		99.0326	PSFFYLSFK	9	22074.6	1000000.0	20.1	1000000.0
mal_4T2c4.pltl		15		99.0216	ILLIRPMLVK	10	1000000.0	1000000.0	95.1	1000000.0
mal_4T2c4.pltl		29		99.0217	LVKLRPMLVK	10	1000000.0	1000000.0	22.3	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
mal_4T2c4.p1t1		36		99.0218	LVKLGPILVK	10	1000000.0	1000000.0	15.0	1000000.0
mal_4T2c4.p1t1		16		99.0327	LLIRPMLVK	9	29115.0	1000000.0	16.1	1000000.0
M13Hg2.q1t3		97		99.0219	LLSRFIFIYK	10	1000000.0	1000000.0	12.9	1000000.0
M13Hg2.q1t3		267		99.0220	KTSDAKLVDK	10	543207.5	1000000.0	21.8	1000000.0
M13Hg2.q1t3		277		99.0221	ETSTISTFIK	10	714638.7	1000000.0	21.8	1000000.0
M13Hg2.q1t3		406		99.0222	IFFSYNPFHK	10	1000000.0	1000000.0	18.5	1000000.0
M13Hg2.q1t3		528		99.0223	YFFNCIQMAK	10	1000000.0	1000000.0	48.6	1000000.0
M13Hg2.q1t3		9		99.0328	SLYNKIEYR	9	32837.9	1000000.0	36.8	1000000.0
M13Hg2.q1t3		48		99.0329	SASESNFYK	9	17208.3	1000000.0	0.2	1000000.0
M13Hg2.q1t3		216		99.0330	ISYIFPLFK	9	12671.6	1000000.0	2.2	1000000.0
M13Hg2.q1t3		420		99.0331	SQNYENINK	9	36248.0	1000000.0	3.6	1000000.0
M13Hg2.q1t3		661		99.0332	SLMDASKNK	9	5327.4	1000000.0	3.2	1000000.0
Mal_5L10c4.q1t6		21		99.0333	KLGFFVCYK	9	42997.2	1000000.0	3.5	1000000.0
Mal_5L10c4.q1t6		36		99.0334	SFKNKILQK	9	139254.7	1000000.0	14.9	1000000.0
Mal_5L10c4.q1t6		56		99.0335	KFMYLRKKK	9	74875.0	1000000.0	33.4	1000000.0
Mal_5L10c4.q1t6		381		99.0336	KQIIFEALK	9	120283.5	1000000.0	38.9	1000000.0
Mal_5L10c4.q1t6		519		99.0337	ETFYKELYK	9	14646.9	1000000.0	1.2	1000000.0
Mal_5L10c4.q1t6		537		99.0338	SVNYFLLER	9	4574.8	1000000.0	0.4	1000000.0
Mal_5L10c4.q1t6		724		99.0339	ILNFLNFNK	9	12039.7	1000000.0	2.7	1000000.0
Mal_5L10c4.q1t6		897		99.0340	NTCSKEIYK	9	26259.6	1000000.0	4.6	1000000.0
Mal_5L10c4.q1t6		1316		99.0341	KLRNFLFYY	9	34.8	1000000.0	27.7	1000000.0
Mal_5L10c4.q1t6		1722		99.0342	CSNNNIFYK	9	16887.2	1000000.0	2.7	1000000.0
571.t00003	Chromosome11	1059		99.0224	MQYNHDNIYK	10	1000000.0	1000000.0	6.8	1000000.0
571.t00003	Chromosome11	2438		99.0225	SFSMLYLFGK	10	1000000.0	1000000.0	20.1	1000000.0
571.t00003	Chromosome11	675		99.0343	ALNPKYQNH	9	4302.1	1000000.0	149.6	1000000.0
571.t00003	Chromosome11	749		99.0344	TLNSFQHNK	9	9140.5	1000000.0	4.0	1000000.0
571.t00003	Chromosome11	1220		99.0345	KINEFQWEK	9	55899.8	1000000.0	0.3	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
571.t00003	Chromosome11	1368		99.0346	RSDYFHNTK	9	15625.8	1000000.0	5.2	1000000.0
571.t00003	Chromosome11	1429		99.0347	STNSQQLIK	9	14992.1	1000000.0	1.1	1000000.0
571.t00003	Chromosome11	1552		99.0348	KFMTPTTLK	9	54389.6	1000000.0	8.1	1000000.0
571.t00003	Chromosome11	1684		99.0349	TTNSTPHFK	9	5905.8	1000000.0	3.8	1000000.0
571.t00003	Chromosome11	2509		99.0350	KLMETRFSK	9	8313.3	1000000.0	2.8	1000000.0
MP03072	PFC0450w	36	CAA15614	99.0226	SQAHRENGKK	10	1000000.0	1000000.0	109.2	1000000.0
MP03072	PFC0450w	45	CAA15614	99.0227	KALVVAIILY	10	220.1	1000000.0	237.1	1000000.0
MP03072	PFC0450w	55	CAA15614	99.0228	VIFLVLLFIY	10	137.2	1000000.0	61.8	1000000.0
MP03072	PFC0450w	56	CAA15614	99.0229	IFLVLLFIYK	10	1000000.0	1000000.0	44.3	1000000.0
MP03072	PFC0450w	58	CAA15614	99.0230	LVLLFIYKAY	10	371.7	1000000.0	207.5	1000000.0
MP03072	PFC0450w	59	CAA15614	99.0231	VLLFIYKAYK	10	1000000.0	1000000.0	31.2	1000000.0
MP03072	PFC0450w	61	CAA15614	99.0232	LFIYKAYKNK	10	1000000.0	1000000.0	434.4	1000000.0
MP03072	PFC0450w	72	CAA15614	99.0233	KLYTNFFMKK	10	1000000.0	1000000.0	5.8	1000000.0
MP03072	PFC0450w	92	CAA15614	99.0234	STYLSASDEY	10	57.2	1000000.0	85.1	1000000.0
MP03072	PFC0450w	36	CAA15614	99.0351	SQAHRENGK	9	65339.9	1000000.0	230.0	1000000.0
MP03072	PFC0450w	46	CAA15614	99.0352	ALVVAIILY	9	6.0	1000000.0	95.4	1000000.0
MP03072	PFC0450w	57	CAA15614	99.0353	FLVLLFIYK	9	14940.5	1000000.0	5.0	1000000.0
MP03072	PFC0450w	58	CAA15614	99.0354	LVLLFIYKA	9	13.1	102.2	132.5	1000000.0
MP03072	PFC0450w	60	CAA15614	99.0355	LLFIYKAYK	9	59055.3	1000000.0	9.6	1000000.0
MP03072	PFC0450w	62	CAA15614	99.0356	FIYKAYKNK	9	35013.8	1000000.0	22.0	1000000.0
MP03072	PFC0450w	72	CAA15614	99.0357	KLYTNFFMK	9	7491.5	1000000.0	2.3	1000000.0
MP03072	PFC0450w	74	CAA15614	99.0358	YTNFFMKKR	9	18478.3	1000000.0	48.4	1000000.0
45.t00001	Chromosome14	50		99.0235	ALERLLSLKK	10	1000000.0	1000000.0	149.5	1000000.0
45.t00001	Chromosome14	109		99.0236	KILIKIPVTK	10	1000000.0	1000000.0	30.2	1000000.0
45.t00001	Chromosome14	128		99.0237	RLPLLPKTWK	10	1000000.0	1000000.0	19.6	1000000.0
45.t00001	Chromosome14	147		99.0238	NIFLRFIPDK	10	1000000.0	1000000.0	24.9	1000000.0
45.t00001	Chromosome14	161		99.0239	SQVSNSDSYK	10	1000000.0	1000000.0	36.0	1000000.0
45.t00001	Chromosome14	197		99.0240	QQNQESKIMK	10	928526.9	1000000.0	431.5	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
45.t00001	Chromosome14	249		99.0241	IIALLIIPPK	10	1000000.0	1000000.0	19.3	1000000.0
45.t00001	Chromosome14	374		99.0242	SQDLACIFDA	10	226.7	389.1	400.3	1000000.0
45.t00001	Chromosome14	34		99.0359	AVIFTPIYY	9	7.6	1000000.0	4.7	1000000.0
45.t00001	Chromosome14	50		99.0360	ALERLLSLK	9	6245.7	1000000.0	55.5	1000000.0
45.t00001	Chromosome14	85		99.0361	SISGKYDIK	9	29562.3	1000000.0	25.1	1000000.0
45.t00001	Chromosome14	101		99.0362	ILCIEGEQK	9	51943.1	1000000.0	162.5	1000000.0
45.t00001	Chromosome14	126		99.0363	EQRLPLLPK	9	66848.0	1000000.0	244.3	1000000.0
45.t00001	Chromosome14	148		99.0364	IFLRFIPDK	9	170326.8	1000000.0	112.0	1000000.0
45.t00001	Chromosome14	250		99.0365	IALLIIPPK	9	47443.5	1000000.0	25.2	1000000.0
45.t00001	Chromosome14	270		99.0366	PVVCSMEYK	9	20870.3	1000000.0	23.1	1000000.0
45.t00001	Chromosome14	271		99.0367	VVCSMEYKK	9	24792.5	1000000.0	8.3	1000000.0
45.t00001	Chromosome14	308		99.0368	FSYDLRLNK	9	5228.9	1000000.0	13.4	1000000.0
45.t00001	Chromosome14	323		99.0369	HLNIPIGFK	9	25082.0	1000000.0	98.3	1000000.0
MP03137	PFC0700c	14	CAB11150	99.0243	SSPLFNNFYK	10	1000000.0	1000000.0	0.5	1000000.0
MP03137	PFC0700c	151	CAB11150	99.0244	FLYLLNKKNK	10	1000000.0	1000000.0	139.2	1000000.0
MP03137	PFC0700c	183	CAB11150	99.0245	LQMMNVNLQK	10	1000000.0	1000000.0	83.6	1000000.0
MP03137	PFC0700c	195	CAB11150	99.0246	LTNHLINTPK	10	427675.0	1000000.0	20.8	1000000.0
MP03137	PFC0700c	259	CAB11150	99.0247	IFISFYLINK	10	1000000.0	1000000.0	102.0	1000000.0
MP03137	PFC0700c	293	CAB11150	99.0248	RLFEESLGIR	10	923199.1	1000000.0	420.0	1000000.0
MP03137	PFC0700c	16	CAB11150	99.0370	PLFNNFYKR	9	11760.5	1000000.0	383.0	1000000.0
MP03137	PFC0700c	141	CAB11150	99.0371	YQNFQNADK	9	40121.5	1000000.0	637.4	1000000.0
MP03137	PFC0700c	184	CAB11150	99.0372	QMMNVNLQK	9	17662.1	1000000.0	1.4	1000000.0
MP03137	PFC0700c	222	CAB11150	99.0373	AVSEIQNNK	9	6991.0	1000000.0	3.1	1000000.0
MP03137	PFC0700c	236	CAB11150	99.0374	GTMYILLKK	9	986.2	1000000.0	0.5	1000000.0
MP03137	PFC0700c	260	CAB11150	99.0375	FISFYLINK	9	7376.0	1000000.0	12.2	1000000.0
MP03137	PFC0700c	264	CAB11150	99.0376	YLINKHWQR	9	39562.3	1000000.0	41.6	1000000.0
MP03137	PFC0700c	273	CAB11150	99.0377	ALKISQLQK	9	37884.8	1000000.0	5.1	1000000.0
MP03137	PFC0700c	282	CAB11150	99.0378	KINSNFLLK	9	5732.3	1000000.0	1.0	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
12.t00018	Chromosome14	89		99.0249	QLKHFFNSNK	10	1000000.0	1000000.0	33.5	1000000.0
12.t00018	Chromosome14	615		99.0250	YVSMYIPFIK	10	301060.0	1000000.0	2.6	1000000.0
12.t00018	Chromosome14	671		99.0251	VLFYIYNMYH	10	900700.0	1000000.0	13.6	1000000.0
12.t00018	Chromosome14	705		99.0252	YTYIFFNYDK	10	742244.6	1000000.0	2.1	1000000.0
12.t00018	Chromosome14	1140		99.0253	SFFITYSYWK	10	1000000.0	1000000.0	5.7	1000000.0
12.t00018	Chromosome14	195		99.0379	STSNKHINR	9	6609.8	1000000.0	3.8	1000000.0
12.t00018	Chromosome14	687		99.0380	SQCNDYYIK	9	95255.3	1000000.0	6.3	1000000.0
12.t00018	Chromosome14	896		99.0381	SSIFYIKNK	9	41588.5	1000000.0	8.4	1000000.0
12.t00018	Chromosome14	1020		99.0382	LFFREKFLK	9	89243.3	1000000.0	14.3	1000000.0
12.t00018	Chromosome14	1160		99.0383	ILDNVSFLK	9	7621.1	1000000.0	21.0	1000000.0
mal_BU121g9.q1c1		10		99.0254	ILVLDIPGFK	10	1000000.0	1000000.0	55.0	1000000.0
mal_BU121g9.q1c1		45		99.0255	ETYGDSLVLH	10	453286.5	1000000.0	386.1	1000000.0
mal_BU121g9.q1c1		59		99.0256	EVGYFKRIFK	10	1000000.0	1000000.0	20.4	1000000.0
mal_BU121g9.q1c1		11		99.0384	LVLDIPGFK	9	13172.2	1000000.0	26.7	1000000.0
mal_BU121g9.q1c1		30		99.0385	GMLTVAGPR	9	54761.5	1000000.0	326.1	1000000.0
mal_BU121g9.q1c1		39		99.0386	SQTELFETY	9	6.7	1000000.0	254.2	1000000.0
mal_BU121g9.q1c1		48		99.0387	GDSLVLHAK	9	19504.9	1000000.0	306.8	1000000.0
mal_BU121g9.q1c1		50		99.0388	SLVLHAKER	9	133501.5	1000000.0	487.4	1000000.0
mal_BU121g9.q1c1		60		99.0389	VGYFKRIFK	9	44416.3	1000000.0	27.9	1000000.0
mal_BU121g9.q1c1		86		99.0390	NIYIYIYIY	9	40.2	1000000.0	322.7	1000000.0
mal_BU121g9.q1c1		88		99.0391	YIYIYIYIY	9	16.2	1000000.0	310.0	1000000.0
mal_9A57b11.q1t2		31		99.0257	SSFNCDIANK	10	1000000.0	1000000.0	8.4	1000000.0
mal_9A57b11.q1t2		49		99.0258	SMGVFCLKEK	10	1000000.0	1000000.0	24.6	1000000.0
mal_9A57b11.q1t2		119		99.0259	HIVKNRIYNK	10	1000000.0	1000000.0	51.7	1000000.0
mal_9A57b11.q1t2		128		99.0260	KLKLHKIIRK	10	1000000.0	1000000.0	64.9	1000000.0
mal_9A57b11.q1t2		165		99.0261	FIFDIFKYAR	10	1000000.0	1000000.0	148.8	1000000.0
mal_9A57b11.q1t2		202		99.0262	AQKALSNLHK	10	1000000.0	1000000.0	113.8	1000000.0
mal_9A57b11.q1t2		208		99.0263	NLHKSWLQYK	10	507559.4	1000000.0	199.6	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC		
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
mal_9A57b11.qlt2		234		99.0264	YLPLFLMMEH	10	1000000.0	1000000.0	147.3	1000000.0
mal_9A57b11.qlt2		32		99.0392	SFNCDIANK	9	27329.1	1000000.0	35.4	1000000.0
mal_9A57b11.qlt2		62		99.0393	KINKKYNKK	9	40379.4	1000000.0	56.4	1000000.0
mal_9A57b11.qlt2		95		99.0394	ILNNKELFK	9	13663.7	1000000.0	29.6	1000000.0
mal_9A57b11.qlt2		120		99.0395	IVKNRIYNK	9	25949.5	1000000.0	17.8	1000000.0
mal_9A57b11.qlt2		154		99.0396	LINSKVFCY	9	6.1	1000000.0	113.8	1000000.0
mal_9A57b11.qlt2		183		99.0397	RQKEFYPIK	9	127059.4	1000000.0	38.7	1000000.0
mal_BL50e8.plca_5		9		99.0265	SFLVVLVFNK	10	1000000.0	1000000.0	33.6	1000000.0
mal_BL50e8.plca_5		152		99.0266	STYMTPSAIK	10	1000000.0	1000000.0	2.8	1000000.0
mal_BL50e8.plca_5		656		99.0267	KLYGEFTMNK	10	1000000.0	1000000.0	1.3	1000000.0
mal_BL50e8.plca_5		907		99.0268	GVYYIFVYLR	10	1000000.0	1000000.0	3.7	1000000.0
mal_BL50e8.plca_5		115		99.0398	SQYSNYFDY	9	11.0	1000000.0	15.2	1000000.0
mal_BL50e8.plca_5		361		99.0399	LFITYFQQK	9	90294.9	1000000.0	50.9	1000000.0
mal_BL50e8.plca_5		409		99.0400	ATSWDEYPK	9	44148.4	1000000.0	0.8	1000000.0
mal_BL50e8.plca_5		752		99.0401	ASFAAHENK	9	11256.9	1000000.0	0.2	1000000.0
mal_BL50e8.plca_5		780		99.0402	MLKADYFIR	9	35925.9	1000000.0	61.1	1000000.0
mal_BL50e8.plca_5		819		99.0403	VLNPVTIPK	9	14931.7	1000000.0	5.6	1000000.0
M13S8h6.plt_3		63		99.0269	VSYIFFMSFK	10	1000000.0	1000000.0	0.4	1000000.0
M13S8h6.plt_3		937		99.0270	MQKYFLHISK	10	1000000.0	1000000.0	37.5	1000000.0
M13S8h6.plt_3		25		99.0404	STFFFFLSR	9	3848.4	1000000.0	0.1	1000000.0
M13S8h6.plt_3		84		99.0405	LLLTFGVYY	9	22.7	1000000.0	157.5	1000000.0
M13S8h6.plt_3		157		99.0406	KFLFRYKQK	9	941796.8	1000000.0	16.1	1000000.0
M13S8h6.plt_3		394		99.0407	KVFIKGKGK	9	43309.1	1000000.0	3.8	1000000.0
M13S8h6.plt_3		1449		99.0408	ITYIWIILK	9	6990.4	1000000.0	1.6	1000000.0
M13S8h6.plt_3		1534		99.0409	KFFFFVFFY	9	51.8	1000000.0	3.5	2.2
M13S8h6.plt_3		1655		99.0410	KLLQKLISK	9	8661.9	1000000.0	53.4	1000000.0
M13S8h6.plt_3		1703		99.0411	ILNILKLAK	9	21447.1	1000000.0	55.0	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
585.t00002	Chromosome11	193		99.0412	SQNNFSKIK	9	90378.2	1000000.0	9.1	1000000.0
585.t00002	Chromosome11	300		99.0413	SSLNIYNTK	9	46908.8	1000000.0	5.2	1000000.0
585.t00002	Chromosome11	529		99.0414	KLFNYKFFK	9	60297.3	1000000.0	1.0	1000000.0
585.t00002	Chromosome11	572		99.0415	LTFLSNIRK	9	13099.9	1000000.0	1.3	1000000.0
585.t00002	Chromosome11	616		99.0416	KFFYIFHYK	9	49030.6	1000000.0	0.2	1000000.0
585.t00002	Chromosome11	1415		99.0417	VTCSYFIIR	9	6831.4	1000000.0	16.8	1000000.0
585.t00002	Chromosome11	1487		99.0418	LTCAFKIYK	9	25752.8	1000000.0	0.3	1000000.0
585.t00002	Chromosome11	1508		99.0419	ILFILFFIK	9	9492.2	1000000.0	1.2	1000000.0
585.t00002	Chromosome11	1541		99.0420	NLYFFIHNR	9	13239.8	1000000.0	59.3	1000000.0
585.t00002	Chromosome11	1742		99.0421	IFLHYYFKK	9	118461.5	1000000.0	7.6	1000000.0
1223.t00015	mal_9A21f9.qlt_4	4294		99.0271	QVFFLQEMER	10	544655.4	1000000.0	27.6	1000000.0
1223.t00015	mal_9A21f9.qlt_4	272		99.0422	SFYKFEVEK	9	193104.9	1000000.0	16.1	1000000.0
1223.t00015	mal_9A21f9.qlt_4	325		99.0423	KTFREHFLK	9	17344.2	1000000.0	0.022	1000000.0
1223.t00015	mal_9A21f9.qlt_4	992		99.0424	VSNSSQLFK	9	13528.2	1000000.0	5.1	1000000.0
1223.t00015	mal_9A21f9.qlt_4	1397		99.0425	SLLNDVFPK	9	67376.3	1000000.0	1.2	1000000.0
1223.t00015	mal_9A21f9.qlt_4	1627		99.0426	KLFIFYLDK	9	25288.3	1000000.0	0.67	1000000.0
1223.t00015	mal_9A21f9.qlt_4	1664		99.0427	LLNSQIIQY	9	18.6	1000000.0	160.0	1000000.0
1223.t00015	mal_9A21f9.qlt_4	2115		99.0428	FQGFYFLDK	9	6204.2	1000000.0	44.3	1000000.0
1223.t00015	mal_9A21f9.qlt_4	2412		99.0429	NTFSFSWMK	9	16414.9	1000000.0	0.20	1000000.0
1223.t00015	mal_9A21f9.qlt_4	4500		99.0430	MFYNCPVYK	9	327575.1	1000000.0	10.3	1000000.0
599.t00001	Chromosome11	723		99.0272	NLLRHAIFYK	10	1000000.0	1000000.0	7.4	1000000.0
599.t00001	Chromosome11	1288		99.0273	SSYGYNIYFK	10	1000000.0	1000000.0	0.3	1000000.0
599.t00001	Chromosome11	1451		99.0274	RTYVNEYFLR	10	1000000.0	1000000.0	25.4	1000000.0
599.t00001	Chromosome11	16		99.0431	ILLTLVFQK	9	46527.3	1000000.0	2.9	1000000.0
599.t00001	Chromosome11	28		99.0432	CQNSLNYSK	9	38238.7	1000000.0	63.2	1000000.0
599.t00001	Chromosome11	211		99.0433	IVNNTELNK	9	9493.8	1000000.0	3.6	1000000.0
599.t00001	Chromosome11	776		99.0434	TLFSQNLFY	9	10.5	1000000.0	75.0	1000000.0
599.t00001	Chromosome11	1320		99.0435	TFYESVFTR	9	63945.9	1000000.0	27.9	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
599.t00001	Chromosome11	1370		99.0436	YFFEEFFNK	9	19717.0	1000000.0	4.6	1000000.0
599.t00001	Chromosome11	1903		99.0437	TTQSNNIYK	9	20011.8	1000000.0	2.1	1000000.0
MP01072	M1045c5.p1c.C_6	1451		99.0275	SLFYFTSNGK	10	1000000.0	1000000.0	8.0	1000000.0
MP01072	M1045c5.p1c.C_6	46		99.0438	KLNYDNFEK	9	48445.0	1000000.0	3.4	1000000.0
MP01072	M1045c5.p1c.C_6	327		99.0439	ILCDDGIYR	9	19413.7	1000000.0	65.3	1000000.0
MP01072	M1045c5.p1c.C_6	359		99.0440	KVADVFLQH	9	6428.6	1000000.0	4.4	1000000.0
MP01072	M1045c5.p1c.C_6	419		99.0441	STSFLFLRK	9	2370.1	1000000.0	0.2	1000000.0
MP01072	M1045c5.p1c.C_6	421		99.0442	SFLFLRKQK	9	408258.6	1000000.0	12.7	1000000.0
MP01072	M1045c5.p1c.C_6	558		99.0443	SFFSSCENK	9	55537.2	1000000.0	17.7	1000000.0
MP01072	M1045c5.p1c.C_6	609		99.0444	AQSSYIYNK	9	18056.8	1000000.0	2.5	1000000.0
MP01072	M1045c5.p1c.C_6	1027		99.0445	MSAKYLYHK	9	5370.6	1000000.0	8.8	1000000.0
MP01072	M1045c5.p1c.C_6	1047		99.0446	TTLFSHFNK	9	10524.0	1000000.0	0.2	1000000.0
MP01072	M1045c5.p1c.C_6	1215		99.0447	SVYYNTMLR	9	9856.9	1000000.0	1.2	1000000.0
PIR2	T28161	1124		99.0276	VVNFLFELYK	10	408697.6	1000000.0	3.5	1000000.0
PIR2	T28161	1403		99.0277	TFFLWDRYKK	10	1000000.0	1000000.0	9.0	1000000.0
PIR2	T28161	108		99.0448	SVGACAPYR	9	59804.6	1000000.0	2.1	1000000.0
PIR2	T28161	204		99.0449	KQLEDNLRK	9	87893.1	1000000.0	16.9	1000000.0
PIR2	T28161	758		99.0450	KVASNMHHK	9	6948.7	1000000.0	1.6	1000000.0
PIR2	T28161	760		99.0451	ASNMHHKKK	9	32965.2	1000000.0	4.3	1000000.0
PIR2	T28161	838		99.0452	AGFISNTYK	9	154161.8	1000000.0	2.2	1000000.0
PIR2	T28161	965		99.0453	ILAFKEIYK	9	14274.5	1000000.0	12.6	1000000.0
PIR2	T28161	1879		99.0454	ALFKRWLEY	9	3.4	1000000.0	27.4	1000000.0
PIR2	T28161	2151		99.0455	AFTYFYLKK	9	40565.6	1000000.0	1.6	1000000.0
55.t00004	Chromosome14	483		99.0278	FFFSNVNNNK	10	409139.5	1000000.0	408.4	1000000.0
55.t00004	Chromosome14	564		99.0279	SQGKKNTYLK	10	1000000.0	1000000.0	13.0	1000000.0
55.t00004	Chromosome14	976		99.0280	VFNNSIILEK	10	1000000.0	1000000.0	372.4	1000000.0
55.t00004	Chromosome14	1338		99.0281	SVSEGYTSTY	10	67.8	1000000.0	33.5	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
55.t00004	Chromosome14	229		99.0456	TSICKYWIK	9	8242.3	1000000.0	14.6	1000000.0
55.t00004	Chromosome14	263		99.0457	TTICKHWKK	9	4558.7	1000000.0	1.7	1000000.0
55.t00004	Chromosome14	537		99.0458	KVTNVHIYK	9	41321.8	1000000.0	0.2	1000000.0
55.t00004	Chromosome14	866		99.0459	ITNMNNINR	9	5371.8	1000000.0	37.6	1000000.0
55.t00004	Chromosome14	909		99.0460	MLNIYKINK	9	17179.3	1000000.0	13.6	1000000.0
55.t00004	Chromosome14	1030		99.0461	IINSYIDYK	9	84561.6	1000000.0	2.0	1000000.0
55.t00004	Chromosome14	1141		99.0462	NLYTYVVNK	9	45076.1	1000000.0	54.8	1000000.0
55.t00004	Chromosome14	1665		99.0463	KMIYSIFIK	9	42191.9	1000000.0	4.1	1000000.0
13.t00011	Chromosome14	8		99.0282	ISMDKSLFFK	10	1000000.0	1000000.0	16.7	1000000.0
13.t00011	Chromosome14	47		99.0283	TVFLDYVKGK	10	1000000.0	1000000.0	7.8	1000000.0
13.t00011	Chromosome14	59		99.0284	DVYKETNMNR	10	1000000.0	1000000.0	64.9	1000000.0
13.t00011	Chromosome14	117		99.0285	KLKKSTICNK	10	1000000.0	1000000.0	59.9	1000000.0
13.t00011	Chromosome14	9		99.0464	SMDKSLFFK	9	4208.2	1000000.0	3.5	1000000.0
13.t00011	Chromosome14	12		99.0465	KSLFFKSLK	9	64105.1	1000000.0	17.4	1000000.0
13.t00011	Chromosome14	48		99.0466	VFLDYVKGK	9	347222.4	1000000.0	216.7	1000000.0
13.t00011	Chromosome14	93		99.0467	KVKRFRVFK	9	52490.3	1000000.0	3.3	1000000.0
13.t00011	Chromosome14	104		99.0468	SFFIDEVKK	9	352606.0	1000000.0	37.8	1000000.0
13.t00011	Chromosome14	112		99.0469	KIYENKLKK	9	30696.4	1000000.0	14.5	1000000.0
37.t00002	Chromosome14	13		99.0286	ALTYMYCVYY	10	249.1	1000000.0	112.8	1000000.0
37.t00002	Chromosome14	31		99.0287	SQISIFCNLR	10	1000000.0	1000000.0	226.6	1000000.0
37.t00002	Chromosome14	32		99.0288	QISIFCNLRR	10	301919.5	1000000.0	80.8	1000000.0
37.t00002	Chromosome14	62		99.0289	VCNNETYYNK	10	1000000.0	1000000.0	186.8	1000000.0
37.t00002	Chromosome14	71		99.0290	KAHEENDKVK	10	1000000.0	1000000.0	956.7	1000000.0
37.t00002	Chromosome14	13		99.0470	ALTYMYCVY	9	9.1	1000000.0	279.6	1000000.0
37.t00002	Chromosome14	32		99.0471	QISIFCNLR	9	26897.2	1000000.0	855.0	1000000.0
37.t00002	Chromosome14	33		99.0472	ISIFCNLRR	9	37287.9	1000000.0	255.9	1000000.0
37.t00002	Chromosome14	61		99.0473	NVCNNETYY	9	25.3	1000000.0	514.8	1000000.0

Table 5:
Pf-derived A3,11 supertype peptides scoring positive on PIC algorithm

Docket No.: EPI-103X

							PIC			
Malaria locus	Addn Source info	Position	Accession No.	Peptide No.	Sequence	AA	A*0101	A*0201 PIC	A*1101 PIC	A*2402
674.t00001	Chromosome11	90		99.0291	LVEFIFLLLK	10	304423.1	1000000.0	13.7	1000000.0
674.t00001	Chromosome11	218		99.0292	SVFYNKEIIK	10	993500.3	1000000.0	4.5	1000000.0
674.t00001	Chromosome11	867		99.0293	SLKDFDMLLY	10	199.3	1000000.0	214.4	1000000.0
674.t00001	Chromosome11	64		99.0474	NVNDRFVEK	9	13728.8	1000000.0	11.8	1000000.0
674.t00001	Chromosome11	662		99.0475	TLSNSLPQK	9	36834.4	1000000.0	47.0	1000000.0
674.t00001	Chromosome11	673		99.0476	YQINNFIHK	9	12103.7	1000000.0	59.8	1000000.0
674.t00001	Chromosome11	689		99.0477	NLTINNFQK	9	59129.2	1000000.0	40.3	1000000.0
674.t00001	Chromosome11	1035		99.0478	KFNRDMLQK	9	254779.4	1000000.0	1.9	1000000.0
674.t00001	Chromosome11	1126		99.0479	NQSDFLLLK	9	8015.9	1000000.0	15.2	1000000.0
674.t00001	Chromosome11	1256		99.0480	SFHHFNIDK	9	178323.3	1000000.0	26.2	1000000.0
674.t00001	Chromosome11	1288		99.0481	KSKELLLQK	9	27230.7	1000000.0	4.4	1000000.0

Table 6:
Pf-derived 15mer peptides with nonamer core sequences scoring DR1 PIC <4nM

Antigen	Addn Source info	Position	Peptide No.	Sequence	AA	DR1 PIC
331.t00003	Chromosome10	182	100.0001	LSHFKKNFILQNNEE	15	0.447
331.t00003	Chromosome10	365	100.0002	TTFLSALKLLKIAQY	15	0.400
331.t00003	Chromosome10	428	100.0003	NNKLSKNLSQLVHFY	15	0.130
331.t00003	Chromosome10	617	100.0004	KIYMFGGFSKGVRNN	15	0.061
331.t00003	Chromosome10	894	100.0005	DDMIGMPNLSSTVVC	15	0.337
331.t00003	Chromosome10	987	100.0006	TFTFQNMYVRSKVVS	15	0.400
331.t00003	Chromosome10	1365	100.0007	KYEIIGNILIFHYKY	15	0.435
331.t00003	Chromosome10	1601	100.0008	KERMKNMYIVSNNDD	15	0.013
331.t00003	Chromosome10	1656	100.0009	GVGYFTLPLLKCIEA	15	0.302
331.t00003	Chromosome10	1725	100.0010	HRIILGLLPHSQPAW	15	0.167
Chr12Contig18	18.000811	13	100.0011	HFFLFLLYILFLVKM	15	1.826
Chr12Contig18	18.000811	16	100.0012	LFLLYILFLVKMNAL	15	0.593
Chr12Contig18	18.000811	21	100.0013	ILFLVKMNALRRLPV	15	0.035
Chr12Contig18	18.000811	27	100.0014	MNALRRLPVICSFLV	15	3.206
Chr12Contig18	18.000811	79	100.0015	SAFLESQSMNKIGDD	15	3.392
Chr12Contig18	18.000811	132	100.0016	LKELIKVGLPSFENL	15	0.785
Chr12Contig18	18.000811	143	100.0017	FENLVAENVKPPKVD	15	0.854
Chr12Contig18	18.000811	148	100.0018	AENVKPPKVDPATYG	15	3.392
Chr12Contig18	18.000811	158	100.0019	PATYGIIVPVLTSLF	15	0.221
Chr12Contig18	18.000811	161	100.0020	YGIIVPVLTSLFNKV	15	0.956
MY924Fe3.pltl		1015	100.0021	SVDLQIKISMKVLNS	15	0.103
MY924Fe3.pltl		1021	100.0022	KISMKVLNSMFHIIM	15	0.234
MY924Fe3.pltl		1076	100.0023	KDVVQIQTVLLSLGF	15	0.066
MY924Fe3.pltl		1331	100.0024	SQIIIILPSILENIL	15	0.092
MY924Fe3.pltl		1526	100.0025	MHSVKEMIVYLIQNN	15	0.262
MY924Fe3.pltl		1703	100.0026	TINLINELMKRQHDK	15	0.192
MY924Fe3.pltl		1746	100.0027	REMLLKMKSMSRNQR	15	0.130
MY924Fe3.pltl		1878	100.0028	RSIIFAGHTIELNSL	15	0.248
MY924Fe3.pltl		1890	100.0029	NSLMFKQTSGRAGRR	15	0.061

Table 6:
Pf-derived 15mer peptides with nonamer core sequences scoring DR1 PIC <4nM

Antigen	Addn Source info	Position	Peptide No.	Sequence	AA	DR1 PIC
MY924Fe3.pltl		2201	100.0030	NLIITYLLIKKVLHN	15	0.162
MP03001	MAL3P2.11	1	100.0031	MRKLAILSVSSFLFV	15	2.786
MP03001	MAL3P2.11	36	100.0032	ELNYDNAGTNLYNEL	15	1.040
MP03001	MAL3P2.11	342	100.0033	QVRIKPGSANKPKDE	15	0.460
1369.t00001	Chromosome 11	28	100.0034	LLKIWKNYMKIMNHL	15	0.328
1369.t00001	Chromosome 11	43	100.0035	MTLYQIQVMKRNQKQ	15	0.056
1369.t00001	Chromosome 11	57	100.0036	QKQVQMMIMIKFMGV	15	0.016
1369.t00001	Chromosome 11	63	100.0037	MIMIKFMGVIYIMII	15	0.545
1369.t00001	Chromosome 11	70	100.0038	GVIYIMIISKKMMRK	15	0.076
1369.t00001	Chromosome 11	285	100.0039	LYYLFNQHIKKELYH	15	0.742
1369.t00001	Chromosome 11	299	100.0040	HFNMLKNKMQSSFFM	15	0.560
1369.t00001	Chromosome 11	353	100.0041	XDIYQKLYIKQEEQK	15	0.807
1369.t00001	Chromosome 11	366	100.0042	QKKYIYNLIMNTQNK	15	0.167
1369.t00001	Chromosome 11	381	100.0043	YEALIKLLPFSKRIR	15	0.701
699.t00001	Chromosome 11	565	100.0044	NIHFAVLFLTLTVYP	15	0.347
699.t00001	Chromosome 11	569	100.0045	AVLFLTLTVYPINNF	15	0.255
699.t00001	Chromosome 11	623	100.0046	KLLYKMNYLKQDINN	15	0.545
699.t00001	Chromosome 11	744	100.0047	KKEFKNSLILLNLYN	15	0.576
699.t00001	Chromosome 11	773	100.0048	YLSFKILNTLLYNHI	15	0.234
699.t00001	Chromosome 11	866	100.0049	IYILINHVIIPSLFY	15	0.400
699.t00001	Chromosome 11	875	100.0050	IPSLFYLYMNFLKFI	15	0.347
699.t00001	Chromosome 11	929	100.0051	KYLIILLYIFKLIEY	15	0.701
699.t00001	Chromosome 11	978	100.0052	FIFMQNNQTKLAEMK	15	0.039
699.t00001	Chromosome 11	1032	100.0053	LFIYIWLHLIIIFIF	15	0.423
mal_4T2c4.pltl		15	100.0054	ILLIRPMLVKLRPKL	15	0.221
mal_4T2c4.pltl		19	100.0055	RPMLVKLRPKLVKLR	15	0.083
mal_4T2c4.pltl		26	100.0056	RPKLVKLRPMLVKLG	15	0.010
mal_4T2c4.pltl		33	100.0057	RPMLVKLGPILVKLR	15	0.004
mal_4T2c4.pltl		40	100.0058	GPILVKLRPMLVKLR	15	0.010

Table 6:
Pf-derived 15mer peptides with nonamer core sequences scoring DR1 PIC <4nM

Antigen	Addn Source info	Position	Peptide No.	Sequence	AA	DR1	PIC
mal_4T2c4.p1t1		47	100.0059	RPMLVKLRPMLAKLR	15		0.016
mal_4T2c4.p1t1		54	100.0060	RPMLAKLRPMLAKLR	15		0.027
mal_4T2c4.p1t1		61	100.0061	RPMLAKLRPKLVKLR	15		0.137
mal_4T2c4.p1t1		68	100.0062	RPKLVKLRPKLVKLR	15		0.083
mal_4T2c4.p1t1		75	100.0063	RPKLVKLRPISVNAK	15		0.076
M13Hg2.q1t3		89	100.0064	ILEMKPNILLSRFIF	15		0.742
M13Hg2.q1t3		122	100.0065	NISINNAFSLPVNIY	15		0.663
M13Hg2.q1t3		163	100.0066	YFNIIQQKIQSNFLL	15		0.487
M13Hg2.q1t3		281	100.0067	ISTFIKNNINHQENN	15		0.682
M13Hg2.q1t3		442	100.0068	LKNMDGNILIKDFIQ	15		0.378
M13Hg2.q1t3		488	100.0069	IEFYNINMAKKVMNN	15		0.285
M13Hg2.q1t3		492	100.0070	NINMAKKVMNNMEKN	15		0.145
M13Hg2.q1t3		558	100.0071	FVNYFEAVVHMNIHC	15		0.831
M13Hg2.q1t3		691	100.0072	NNNIINGHMLEQKLS	15		0.123
M13Hg2.q1t3		869	100.0073	NNDMKKGYTNVSNNS	15		0.162
Mal_5L10c4.q1t6		154	100.0074	NNEFFGYPLQFVCET	15		0.255
Mal_5L10c4.q1t6		336	100.0075	FFIIKNVGVHKITYY	15		0.388
Mal_5L10c4.q1t6		1090	100.0076	KIEYISMLSPTINEI	15		0.113
Mal_5L10c4.q1t6		1101	100.0077	INEIKTLNTILTIPL	15		0.018
Mal_5L10c4.q1t6		1107	100.0078	LNTILTIPLIKMNEY	15		0.042
Mal_5L10c4.q1t6		1264	100.0079	HKLFINKLMTSNIRK	15		0.203
Mal_5L10c4.q1t6		1289	100.0080	QNRFRNQLLYLTKIA	15		0.050
Mal_5L10c4.q1t6		1609	100.0081	IKKIKTPLILPIDPN	15		0.035
Mal_5L10c4.q1t6		1888	100.0082	QDHLVIQIIYVMDNI	15		0.133
Mal_5L10c4.q1t6		2031	100.0083	IEAMGGAHSIGYEQF	15		0.068
571.t00003	Chromosome11	33	100.0084	FDDFKINYSYKTKNH	15		0.182
571.t00003	Chromosome11	462	100.0085	ITDLNNMNVNQSNMK	15		0.500
571.t00003	Chromosome11	960	100.0086	TNNFNNNVMMLMNTS	15		0.007
571.t00003	Chromosome11	1124	100.0087	EQNVAQNVAQNVAQN	15		0.460

Table 6:
Pf-derived 15mer peptides with nonamer core sequences scoring DR1 PIC <4nM

Antigen	Addn Source info	Position	Peptide No.	Sequence	AA	DR1	PIC
571.t00003	Chromosome11	1128	100.0088	AQNVAQNVAQNVEQN	15		0.460
571.t00003	Chromosome11	1550	100.0089	SNKFMTPTTLKEKYQ	15		0.255
571.t00003	Chromosome11	1941	100.0090	NIHMINDVATKLNQH	15		0.285
571.t00003	Chromosome11	2112	100.0091	HIHMMNQQIQKETNT	15		0.576
571.t00003	Chromosome11	2255	100.0092	NNVFQQPLSYSNGSE	15		0.347
571.t00003	Chromosome11	2738	100.0093	NNTINMNGMNKTESI	15		0.198
MP03072	PFC0450w	5	100.0094	LNILILIDAASVAFL	15		0.722
MP03072	PFC0450w	8	100.0095	LILIDAASVAFLLIT	15		1.340
MP03072	PFC0450w	17	100.0096	AFLLITFLMINLNEE	15		1.197
MP03072	PFC0450w	44	100.0097	KKALVVAIILYVIFL	15		0.302
MP03072	PFC0450w	48	100.0098	VVAIILYVIFLVLLF	15		0.609
MP03072	PFC0450w	52	100.0099	ILYVIFLVLLFIYKA	15		0.831
MP03072	PFC0450w	55	100.0100	VIFLVLLFIYKAYKN	15		0.956
MP03072	PFC0450w	58	100.0101	LVLLFIYKAYKNKRK	15		4.016
MP03072	PFC0450w	76	100.0102	NFFMKKRNAPKYVQL	15		0.593
MP03072	PFC0450w	85	100.0103	PKYVQLASTYLSASD	15		2.865
45.t00001	Chromosome14	2	100.0104	ENEYATGAVRPFQAA	15		0.722
45.t00001	Chromosome14	27	100.0105	NYELSKKAVIFTPIY	15		1.197
45.t00001	Chromosome14	108	100.0106	QKILIKIPVTKNIIT	15		0.085
45.t00001	Chromosome14	156	100.0107	KCLVISQVSNSDSYK	15		2.044
45.t00001	Chromosome14	202	100.0108	SKIMKLPKLPISNGK	15		0.742
45.t00001	Chromosome14	220	100.0109	FIHFFTWGTMFVPKY	15		0.026
45.t00001	Chromosome14	242	100.0110	LCNFKKNIIALLIIP	15		0.203
45.t00001	Chromosome14	246	100.0111	KKNIIALLIIPPKIH	15		0.010
45.t00001	Chromosome14	251	100.0112	ALLIIPPKIHISIEL	15		1.267
45.t00001	Chromosome14	274	100.0113	SMEYKKDFLITARKP	15		1.826
MP03137	PFC0700c	7	100.0114	KSKFNILSSPLFNNF	15		1.987
MP03137	PFC0700c	173	100.0115	FKKLKNHVLFLQMMN	15		0.785
MP03137	PFC0700c	177	100.0116	KNHVLFLQMMNVNLQ	15		0.095

Table 6:
Pf-derived 15mer peptides with nonamer core sequences scoring DR1 PIC <4nM

Docket No.: EPI-103X

Antigen	Addn Source info	Position	Peptide No.	Sequence	AA	DR1	PIC
MP03137	PFC0700c	180	100.0117	VLFLQMMNVNLQKQL	15		0.068
MP03137	PFC0700c	187	100.0118	NVNLQKQLLTNHLIN	15		0.956
MP03137	PFC0700c	191	100.0119	QKQLLTNHLINTPKI	15		1.132
MP03137	PFC0700c	197	100.0120	NHLINTPKIMPHHII	15		0.576
MP03137	PFC0700c	239	100.0121	YILLKKILSSRFNQM	15		1.100
MP03137	PFC0700c	250	100.0122	FNQMIFVSSIFISFY	15		2.420
12.t00018	Chromosome14	36	100.0123	CNILKENNTYKQKKH	15		4.016
12.t00018	Chromosome14	133	100.0124	TNELKKMDTKKDVHM	15		1.011
12.t00018	Chromosome14	504	100.0125	EVKFILHMTLLTLYK	15		0.269
12.t00018	Chromosome14	542	100.0126	KYNFLNIYASLRNEY	15		0.328
12.t00018	Chromosome14	583	100.0127	TRCFKNSYPKKVWKK	15		0.293
12.t00018	Chromosome14	612	100.0128	NNLYVSMYIPFIKKF	15		0.411
12.t00018	Chromosome14	1000	100.0129	EAKFKIERLLKSSYK	15		3.298
12.t00018	Chromosome14	1057	100.0130	KIYILNNNLLIVHLS	15		1.543
12.t00018	Chromosome14	1184	100.0131	KCSFDKTNPIQQSGK	15		2.044
12.t00018	Chromosome14	1212	100.0132	TGIFNMPNLVQINNY	15		0.078
mal_BU121g9.q1c1		29	100.0133	EGMLTVAGPRSQTEL	15		3.298
mal_9A57b11.q1t2		3	100.0134	KQNIKYTQIISIDNI	15		2.633
mal_9A57b11.q1t2		18	100.0135	LNKIADPILIGFSSS	15		0.929
mal_9A57b11.q1t2		123	100.0136	NRIYNKLKLHKIIRK	15		1.267
mal_9A57b11.q1t2		194	100.0137	NNEYGILNAQKALSN	15		0.098
mal_9A57b11.q1t2		197	100.0138	YGILNAQKALSNLHK	15		0.141
mal_9A57b11.q1t2		229	100.0139	KIFVKYLPLFLMMEH	15		0.042
mal_9A57b11.q1t2		236	100.0140	PLFLMMEHSFLNCHK	15		3.031
mal_BL50e8.p1ca_5		1	100.0141	MEGFVALLSFLVVLV	15		0.004
mal_BL50e8.p1ca_5		100	100.0142	VDGMKIGHPISVALG	15		0.010
mal_BL50e8.p1ca_5		151	100.0143	GSTYMTPSAIKIKVP	15		0.057
mal_BL50e8.p1ca_5		189	100.0144	NNLFIYNWVLQTSSP	15		0.560
mal_BL50e8.p1ca_5		347	100.0145	EKILIRALLSLDFSL	15		0.722

Table 6:
Pf-derived 15mer peptides with nonamer core sequences scoring DR1 PIC <4nM

Antigen	Addn Source info	Position	Peptide No.	Sequence	AA	DR1 PIC
mal_BL50e8.plca_5		437	100.0146	HPVYPTAPAVAFPAG	15	0.187
mal_BL50e8.plca_5		585	100.0147	EVYYFPGKVTRVRAK	15	0.357
mal_BL50e8.plca_5		606	100.0148	EDKLVKIYISLLSSD	15	0.423
mal_BL50e8.plca_5		685	100.0149	IERYVGLGSFHFYLY	15	0.423
mal_BL50e8.plca_5		816	100.0150	CFQVLNPVTIPKYCI	15	0.285
M13S8h6.plt_3		68	100.0151	FMSFKILEALLVCIS	15	0.006
M13S8h6.plt_3		127	100.0152	KQIVIFLISLLSFTL	15	0.473
M13S8h6.plt_3		169	100.0153	AKQIEILHTMLPNFL	15	0.095
M13S8h6.plt_3		218	100.0154	IDDFQNMVSTLQPHV	15	0.034
M13S8h6.plt_3		285	100.0155	KCAIKLAIAQLSAKY	15	0.130
M13S8h6.plt_3		343	100.0156	IGSVKPQYALFGDTV	15	0.228
M13S8h6.plt_3		871	100.0157	KIYIKKKRLLQMNNY	15	0.411
M13S8h6.plt_3		1350	100.0158	KKLLKKLTSNLQLNK	15	0.076
M13S8h6.plt_3		1602	100.0159	QDFLTKILPRQVLEE	15	0.241
M13S8h6.plt_3		1754	100.0160	MWGLDVLIANKIESN	15	0.423
585.t00002	Chromosome11	5	100.0161	FFILFYFYVMSTYTF	15	0.500
585.t00002	Chromosome11	16	100.0162	TYTFCFLPVLQTQLG	15	0.515
585.t00002	Chromosome11	349	100.0163	KKKYKNKKMPKTIDG	15	0.473
585.t00002	Chromosome11	487	100.0164	GRAIIPLFLILNTYK	15	0.269
585.t00002	Chromosome11	562	100.0165	KIIFKRNPLFLTFLS	15	0.367
585.t00002	Chromosome11	643	100.0166	WLFFFDLVVLSPFSL	15	0.500
585.t00002	Chromosome11	774	100.0167	KNIIKGKNMMTRGGG	15	0.106
585.t00002	Chromosome11	796	100.0168	KMFIKGDTVMKANII	15	0.038
585.t00002	Chromosome11	1093	100.0169	VGSYKLMISQEAEFE	15	0.487
585.t00002	Chromosome11	1344	100.0170	LNRFITLITWTQHVS	15	0.095
1223.t00015	mal_9A21f9.qlt_4	1070	100.0171	RTKYETLVTIHVHQR	15	0.087
1223.t00015	mal_9A21f9.qlt_4	1162	100.0172	GLCYGGAPAGPAGTG	15	0.059
1223.t00015	mal_9A21f9.qlt_4	1654	100.0173	DSILILQTINLLNSQ	15	0.177
1223.t00015	mal_9A21f9.qlt_4	2461	100.0174	KHLIIINRVMQTPNG	15	0.043

Table 6:
Pf-derived 15mer peptides with nonamer core sequences scoring DR1 PIC <4nM

Antigen	Addn Source info	Position	Peptide No.	Sequence	AA	DR1 PIC
1223.t00015	mal_9A21f9.qlt_4	2779	100.0175	IDLYKQMYVKKYDEI	15	0.158
1223.t00015	mal_9A21f9.qlt_4	2878	100.0176	DKDLKAALPYLHEAE	15	0.103
1223.t00015	mal_9A21f9.qlt_4	2985	100.0177	TIELLKPYIQSTFFK	15	0.145
1223.t00015	mal_9A21f9.qlt_4	2995	100.0178	STFFKTQIAKKASVA	15	0.002
1223.t00015	mal_9A21f9.qlt_4	3014	100.0179	CKWVGAMAMYNQASK	15	0.145
1223.t00015	mal_9A21f9.qlt_4	3019	100.0180	AMAMYNQASKIVKPK	15	0.116
599.t00001	Chromosome11	12	100.0181	INFFILLTLVFQKYS	15	0.177
599.t00001	Chromosome11	364	100.0182	NNNLGIPTLIKKEVH	15	0.234
599.t00001	Chromosome11	519	100.0183	EEDIKNAYLPENKNF	15	0.435
599.t00001	Chromosome11	1074	100.0184	INVFIKEISKLFDHD	15	0.529
599.t00001	Chromosome11	1414	100.0185	DKSLKIMYSLFNKYT	15	0.098
599.t00001	Chromosome11	1463	100.0186	VVIFIYGNIIISDLK	15	0.645
599.t00001	Chromosome11	1621	100.0187	CESFISKVTNKVIKK	15	0.215
599.t00001	Chromosome11	1740	100.0188	ICTFVKYITFQLLNI	15	0.854
599.t00001	Chromosome11	1767	100.0189	KEHYIMNNTIFTFNQ	15	0.141
599.t00001	Chromosome11	1892	100.0190	KKKYKYIPSNGTTQS	15	0.500
M1045c5.plc.C_6		53	100.0191	EKSLGILGSIQNAYL	15	0.085
M1045c5.plc.C_6		59	100.0192	LGSIQNAYLYKSIFK	15	0.388
M1045c5.plc.C_6		588	100.0193	SCIMNNMIVTKESNE	15	0.473
M1045c5.plc.C_6		1040	100.0194	KDFMKNNTTLFSHFN	15	0.241
M1045c5.plc.C_6		1136	100.0195	MLYLIRNILMSIEDY	15	0.435
M1045c5.plc.C_6		1229	100.0196	KKKYIKLNIFKNIIL	15	0.378
M1045c5.plc.C_6		1350	100.0197	RWDLVMNMMIGIRIS	15	0.054
M1045c5.plc.C_6		1380	100.0198	HKDVIQLPTSNAQHK	15	0.167
M1045c5.plc.C_6		1393	100.0199	HKVIFKNYAPIIFKN	15	0.262
M1045c5.plc.C_6		1430	100.0200	SNMVLGNLSTLSELL	15	0.423
PIR2	T28161	46	100.0201	AKFYNGGEIMQPNSK	15	0.153
PIR2	T28161	319	100.0202	KRNLKLQNAIKNCRG	15	0.043
PIR2	T28161	1072	100.0203	HVKIIKNLLIHGKEQ	15	0.302

Table 6:
Pf-derived 15mer peptides with nonamer core sequences scoring DR1 PIC <4nM

Antigen	Addn Source info	Position	Peptide No.	Sequence	AA	DR1	PIC
PIR2	T28161	1093	100.0204	KYKLLYLQAQTTAAN	15	0.141	
PIR2	T28161	1096	100.0205	LLYLQAQTTAANGGP	15	0.047	
PIR2	T28161	1589	100.0206	SPKIVVPAPKPTTTF	15	0.119	
PIR2	T28161	1951	100.0207	FVDLIRQIAATIDKG	15	0.047	
PIR2	T28161	2065	100.0208	QERLVKNPLVQPTLK	15	0.028	
PIR2	T28161	2129	100.0209	HPAVIPALVTSTLAW	15	0.072	
PIR2	T28161	2419	100.0210	NELFGTNHVKQTSIH	15	0.098	
55.t00004	Chromosome14	81	100.0211	NNEFVVAQLYELNNY	15	1.340	
55.t00004	Chromosome14	117	100.0212	DNNMKKYLIQKCGKK	15	1.776	
55.t00004	Chromosome14	218	100.0213	SCSIIKYELRKTSIC	15	1.878	
55.t00004	Chromosome14	385	100.0214	RNHMDKPPPHNINNN	15	0.228	
55.t00004	Chromosome14	613	100.0215	NNNLIFQNSRFMDHT	15	0.423	
55.t00004	Chromosome14	754	100.0216	THDIIKNVSNNMKRF	15	0.357	
55.t00004	Chromosome14	904	100.0217	FKNVDMLNIYKINKD	15	1.987	
55.t00004	Chromosome14	1136	100.0218	MKDVINLYTYVVNKK	15	0.092	
55.t00004	Chromosome14	1364	100.0219	GMYILPQYVTRECIN	15	1.500	
55.t00004	Chromosome14	1510	100.0220	GDDVIYEETKKTDNI	15	1.587	
13.t00011	Chromosome14	16	100.0221	FKSLKNNNMLESTGI	15	1.587	
13.t00011	Chromosome14	49	100.0222	FLDYVKGKMMDVYKE	15	0.126	
13.t00011	Chromosome14	84	100.0223	TYNYLTPTLKVKRFR	15	3.589	
37.t00002	Chromosome14	50	100.0224	NDLIDQNIVYLNVCN	15	2.560	
674.t00001	Chromosome11	30	100.0225	LKKLKKILLNLDVLI	15	0.742	
674.t00001	Chromosome11	54	100.0226	NENFDMELLNNVNDR	15	1.378	
674.t00001	Chromosome11	124	100.0227	NCPIKNEVTTLIQKI	15	0.367	
674.t00001	Chromosome11	296	100.0228	EKNMTSQKSITSEKN	15	0.854	
674.t00001	Chromosome11	577	100.0229	NSNFKEQHLLFCNNL	15	1.418	
674.t00001	Chromosome11	752	100.0230	NNNIKTHIANFNIIH	15	1.040	
674.t00001	Chromosome11	986	100.0231	NNLYKTYEMIQGDND	15	0.956	
674.t00001	Chromosome11	1093	100.0232	NDNYINNNIYLNKAN	15	1.340	

Table 6:
Pf-derived 15mer peptides with nonamer core sequences scoring DR1 PIC <4nM

Antigen	Addn Source info	Position	Peptide No.	Sequence	AA	DR1	PIC
674.t00001	Chromosome11	1353	100.0233	FLQYRIPHMNNNGNI	15	0.983	
674.t00001	Chromosome11	1432	100.0234	VDIFCKIHALKNENK	15	0.854	